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                    GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:     December 20, 2002, 16:20:40 ; Search time 17 Seconds
                               (without alignments)
                               3688.953 Million cell updates/sec

Title:       US-09-697-898-2
Perfect score: 7825
Sequence:    1 MAAAAGNRASSSGFPGARAT.........PQDRPPSRELLKHPVFRTTW 1512

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:    112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:     112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_40:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7515	96.0	1495	1	M3K1_HUMAN	Q13233 homo sapien
2	6920.5	88.4	1493	1	M3K1_MOUSE	P53349 mus musculu
3	6892.5	88.1	1493	1	M3K1_RAT	Q62925 rattus norv
4	619	7.9	1478	1	BCK1_YEAST	Q01389 saccharomyc
5	559	7.1	626	1	M3K3_MOUSE	Q61084 mus musculu
6	558.5	7.1	626	1	M3K3_HUMAN	Q99759 homo sapien
7	543.5	6.9	659	1	BYR2_SCHPO	P28829 schizosacch
8	535.5	6.9	618	1	M3K2_HUMAN	Q9Y2U5 homo sapien
9	535	6.8	738	1	STI1_YEAST	P23561 saccharomyc
10	531	6.8	619	1	M3K2_MOUSE	Q61083 mus musculu
11	517.5	6.6	1116	1	MKH1_SCHPO	Q10407 schizosacch
12	502.5	6.4	1607	1	M3K4_HUMAN	Q9Y6R4 homo sapien
13	475	6.1	1597	1	M3K4_MOUSE	Q08648 mus musculu
14	433.5	5.5	1401	1	WIS4_SCHPO	Q14299 schizosacch
15	430.5	5.5	1374	1	M3K5_HUMAN	Q99683 homo sapien
16	429.5	5.5	1379	1	M3K5_MOUSE	O35099 mus musculu
17	423	5.4	1579	1	SSK2_YEAST	P53599 saccharomyc
18	410	5.2	1436	1	WIN1_SCHPO	O74304 schizosacch
19	408.5	5.2	1011	1	M3K6_HUMAN	O95382 homo sapien
20	398.5	5.1	658	1	PAK1_SCHPO	P50527 schizosacch
21	388.5	5.0	939	1	ST20_YEAST	Q03497 saccharomyc
22	387.5	5.0	544	1	PAK3_HUMAN	O75914 homo sapien
23	379	4.8	545	1	PAK1_MOUSE	O88643 mus musculu
24	378.5	4.8	524	1	PAK1_RABIT	Q29502 oryctolagus
25	377.5	4.8	544	1	PAK3_RAT	Q62829 rattus norv
26	377.5	4.8	545	1	PAK1_HUMAN	Q13153 homo sapien
27	377	4.8	544	1	PAK1_RAT	P35465 rattus norv
28	375.5	4.8	426	1	ST25_MOUSE	Q922w1 mus musculu
29	374.5	4.8	524	1	PAK2_HUMAN	Q13177 homo sapien
30	373.5	4.8	1062	1	CC7_SCHPO	P41892 schizosacch
31	373.5	4.8	1230	1	ST20_CANAL	Q92212 candida alb
32	371	4.7	942	1	M3KE_MOUSE	Q9wu16 mus musculu
33	370.5	4.7	426	1	ST25_HUMAN	O00506 homo sapien
34	367.5	4.7	524	1	PAK2_RAT	Q64303 rattus norv
35	366.5	4.7	544	1	PAK3_MOUSE	Q61036 mus musculu
36	364	4.6	443	1	ST24_HUMAN	Q9y6e0 homo sapien
37	360.5	4.6	288	1	PEF1_SCHPO	O74456 schizosacch
38	360	4.6	646	1	CNK_HUMAN	Q9h4b4 homo sapien
39	359.5	4.6	631	1	CNK_MOUSE	Q60806 mus musculu
40	359.5	4.6	1314	1	SS22_YEAST	P25390 saccharomyc
41	355	4.5	947	1	M3KE_HUMAN	Q99558 homo sapien
42	352.5	4.5	384	1	ARK1_SCHPO	O59790 schizosacch
43	352	4.5	615	1	CNK_RAT	Q9r011 rattus norv
44	350	4.5	1914	1	KMLS_HUMAN	Q15746 homo sapien
45	347	4.4	974	1	CC15_YEAST	P27636 saccharomyc

ALIGNMENTS

```
RESULT 1
M3K1_HUMAN
ID   M3K1_HUMAN           STANDARD;     PRT;   1495 AA.
AC   Q13233;
DT   01-NOV-1997 (Rel. 35, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.1.-)
DE   (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1) (Fragment).
GN   MAP3K1 OR MAPKKK1 OR MEKK1 OR MEKK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99026111; PubMed=9808624;
RA   Xia Y., Wu Z., Su B., Murray B., Karin M.;
RT   "JNKK1 organizes a MAP kinase module through specific and sequential
RT   interactions with upstream and downstream components mediated by its
RT   amino-terminal extension.";
RL   Genes Dev. 12:369-381(1998).
RN   [2]
RP   SEQUENCE OF 1221-1257 FROM N.A.
RC   TISSUE=Leukocyte;
RX   MEDLINE=96169565; PubMed=8597633;
RA   Vinik B.S., Kay E.S., Fiedorek F.T.;
RT   "Mapping of the MEK kinase gene (Mekk) to mouse chromosome 13 and
RT   human chromosome 5.";
RL   Mamm. Genome 6:782-783(1995).
CC   -!- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE MAPKK 1 AND MAPKK 2
CC       (MEK1/MEK2) WHICH LEADS TO PHOSPHORYLATION OF MAP KINASES. IT IS
CC       ALSO A HIGHLY EFFICIENT ACTIVATOR OF THE JNK CASCADE.
CC   -!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- MAP KINASE KINASE KINASE SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   --------------------------------------------------------------------------
DR   EMBL; AF042838; AAC97073.1; -.
DR   EMBL; U29671; AAB05828.1; -.
DR   HSSP; Q00534; 1B17.
DR   SWISS-2DPAGE; Q13233; HUMAN.
DR   Genew; HGNC:6848; MAP3K1.
DR   MIM; 600982; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000290; Ser_thr_pkinase.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00069; pkinase; 1.
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DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; zinc-finger.
FT   NON_TER       1       1
FT   ZN_FING     424     473     RING-TYPE.
FT   DOMAIN     1226    1491     PROTEIN KINASE.
FT   DOMAIN      403     412     POLY-SER.
FT   DOMAIN      925     932     POLY-THR.
FT   DOMAIN     1165    1170     POLY-GLU.
FT   NP_BIND    1232    1239     ATP (BY SIMILARITY).
FT   BINDING    1255    1255     ATP (BY SIMILARITY).
FT   ACT_SITE   1352    1352     BY SIMILARITY.
SQ   SEQUENCE   1495 AA;  163653 MW;  2D6ECB52E7AFC4B CRC64;

Query Match     96.0%;
Best Local Similarity   97.8%;        Score 7515;  DB 1;  Length 1495;
Matches 1461;  Conservative  3;  Mismatches 28;  Indels 28;  Gaps 2;        Pred. No. 1.2e-308;
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Qy   21 SPEAGGGGALKASSAPAAAAGLLREAGSGGREADWRRRQLRKVRSVELDQLPEQPLFL 80
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Db    2 SPEAGGGGGALKASSARAAAAGLLREAGSGGREADWRRRQLRKVRSVELDQLPEQPLFL 61

Qy   81 AASPPASSTSPSPEPADAAGSGTGFQPVAVPPHGAASRGGAHLTESVAAPDSGASSPAA 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 AASPPASSTSPSPEPADAAGSGTGFQPVAVPPHGAASRGGAHLTESVAAPDSGASSPAA 121

Qy  141 AEPGEKRAPAAEPSPAAAPAGREMENKETLKGLHKMDDRPEERMIREKLKATCMPAWKHE 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  122 AEPGEKRAPAAEPSPAAAPAGREMENKETLKGLHKMDDRPEERMIREKLKATCMPAWKHE 181

Qy  201 WLERRNRRGPVVVKPIPVKGDGSEMNHLAAESPGEVQASAASKGRRSPSPGNSPSGR 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  182 WLERRNRRGPVVVKPIPVKGDGSEMNHLAAESPGEVQASAASKGRRSPSPGNSPSGR 241

Qy  261 TVKSESPGVRRKRVSPVPFQSGRITPPRRAPSPDGFSPYSPEETNRRVNKVMRARLYLLQ 320
          ||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db  242 TVKSESPGVRRKRVSPVPFQSGRITPPRRAPSPDGFSPYSPEETNRRVNKVMRARLYLLQ 301

Qy  321 QIGPNSFLIGGDSPDNKYRVFIGPQNCSCARGTFCIHLLFVMLRVFQLEPSDPMLWRKTL 380
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  302 QIGPNSFLIGGDSPDNKYRVFIGPQNCSCAHGTFCIHLLFVMLRVFQLEPSDPMLWRKTL 361

Qy  381 KNFEVESLFQKYHSRRSSRIKAPSRNTIQKFVSRMSNSHTLSSSSTSTSSSENSIKDEEE 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  362 KNFEVESLFQKYHSRRSSRIKAPSRNTIQKFVSRMSNSHTLSSSSTSTSSSENSIKDEEE 421

Qy  441 QMCPICLLGMLDEESLTVCEDGCRNKLHHCMSIWAEECRRNREPLICPLCRSKWRSHDF 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  422 QMCPICLLGMLDEESLTVCEDGCRNKLHHCMSIWAEECRRNREPLICPLCRSKWRSHDF 481

Qy  501 YSHELSSPVDSPSSLRAAQQQTVQQQPLAGSRRNQESNFNLTHYGTQQIPPAYKDLAEPW 560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  482 YSHELSSPVDSPSSLRAAQQQTVQQQPLAGSRRNQESNFNLTHYGTQQIPPAYKDLAEPW 541

Qy  561 IQVFGMELVGCLFSRNWNVREMALRRLSHDVSGALLLANGESTGNSGGSGSGSPSGGATS 620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  542 IQVFGMELVGCLFSRNWNVREMALRRLSHDVSGALLLANGESTGNSGGSGSGSPSGGATS 601

Qy  621 GSSQTSISGDVVEACCSVLSMVCADPVYKVYVAALKTLRAMLVTPCHSLAERIKLQRLL 680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  602 GSSQTSISGDVVEACCSVLSMVCADPVYKVYVAALKTLRAMLVTPCHSLAERIKLQRLL 661

Qy  681 QPVVDTILVKCADANSRTSQLSISTLLELCKGQAGELAVGREILKAGSIGIGGVDYVLNC 740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  662 QPVVDTILVKCADANSRTSQLSISTLLELCKGQAGELAVGREILKAGSIGIGGVDYVLNC 721
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Qy  741 ILGNQTESNNWQELLGRLCLIDRLLLEFPAEFYPHIVSTDVSQAEPVEIRYKKLLSLLTF 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  722 ILGNQTESNNWQELLGRLCLIDRLLLEFPAEFYPHIVSTDVSQAEPVEIRYKKLLSLLTF 781

Qy  801 ALQSIDNSHSMVGKLSRRIYLSSARMVTTVPHVFSKLLEMLSVSS-STHFTRMRRRLMAI 859
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  782 ALQSIDNSHSMVGKLSRRIYLSSARMVTTVPHVFSKLLEMLSVSSVSTHFTRMRRRLMAY 841

Qy  860 ADEVEIAEAIQLGVEDTLDGQQ-DSFLQASVPNNYLETTENSSPECTVHLEKTGKGLCAT 918
          ||||||||||||||||| :  : :::  :        |||||||||||||||||||||
Db  842 ADEVEIAEAIQLGVEDTLQRQQHSFCRHLFPTIIWKPQRTVPLECTVHLEKTGKGLCAT 901

Qy  919 KLSASSEDISERLASISVGPSSSTTTTTTTEQPKPMVQTKGRPHSQCLNSSPLSHHSQL 978
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db  902 KLSASSEDISERLARISVGPSSSTTTTTTTEQPKPMVQTKGRPHSQCLNSSPLSHHSQL 961

Qy  979 MFPALSTPSSSTPSVPAGTATDVSKHRLQGFIPCRIPSASPQTQRKFSLQFHRNCPENKD 1038
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  962 MFPALSTPSSSTPSVPAGTATDVSKHRLQGFIPCRIPSASPQTQRKFSLQFHRNCPENKD 1021

Qy 1039 SDKLSPVFTQSRPLPSSNIHRPKPSRPTPGNTSKQGDPSKNSMTLDLNSSSKCDDSFGCS 1098
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db 1022 SDKLSPVFTQSRPLPSSNIHRPKPSRPTPGNTSKQGDPSKNSMTLDLNSSSKCDDSFGLS 1081

Qy 1099 SNSSNAVIPSDETVFTPVEEKCRLDVNTELNSSIEDLLEASMPSSDTTVTFKSEVAVLSP 1158
          ||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1082 SNSSNCCYTSDETVFTPVEEKCRLDVNTELNSSIEDLLEASMPSSDTTVTFKSEVAVLSP 1141

Qy 1159 EKAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSASQDALPIVPQLQVENGEDIII 1218
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db 1142 EKAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSASQVALPIVPQLQVENGEDIII 1201

Qy 1219 IQQDTPETLPGHTKAKQPYREDTEWLKGQQIGLGAFSSCYQAQDVGTGLMAVKQVTYVR 1278
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1202 IQQDTPETLPGHTKAKQPYREDTEWLKGQQIGLGAFSSCYQAQDVGTGLMAVKQVTYVR 1261

Qy 1279 NTSSEQEVVEALREEIRMSHLNHPNIIRMLGATCEKSNYNLFIEWMAGGSVAHLLSKY 1338
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1262 NTSSEQEVVEALREEIRMSHLNHPNIIRMLGATCEKSNYNLFIEWMAGGSVAHLLSKY 1321

Qy 1339 GAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIADFGAAARLASK 1398
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1322 GAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIADFGAAARLASK 1381

Qy 1399 GTGAGEFQGQLLGTIAFMAPEVLRGQQYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHL 1458
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1382 GTGAGEFQGQLLGTIAFMAPEVLRGQQYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHL 1441

Qy 1459 ALIFKIASATTAPSIPSHLSPGLRDVALRCLELQPQDRPPSRELLKHPVFRTTW 1512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1442 ALIFKIASATTAPSIPSHLSPGLRDVALRCLELQPQDRPPSRELLKHPVFRTTW 1495
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RESULT 2
M3K1_MOUSE
ID   M3K1_MOUSE     STANDARD;     PRT;   1493 AA.
AC   P53349; Q60831; Q9R256; Q9R0U3;
DT   01-OCT-1996 (Rel. 34, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.1.-)
DE   (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1).
GN   MAP3K1 OR MEKK1 OR MEKK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lange C.A., Blumer K.J., Sather S.L., Johnson G.L.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-659 FROM N.A.
```

```
RC   TISSUE=Spleen;
RX   MEDLINE=99455010; PubMed=10523642;
RA   Ito M., Yoshioka K., Akechi M., Yamashita S., Takamatsu N.,
RA   Sugiyama K., Hibi M., Nakabeppu Y., Shiba T., Yamamoto K.-I.;
RT   "JSAP1, a novel jun N-terminal protein kinase (JNK)-binding protein
RT   that functions as a scaffold factor in the JNK signaling pathway.";
RL   Mol. Cell. Biol. 19:7539-7548(1999).
RN   [3]
RP   SEQUENCE OF 660-1493 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=93227040; PubMed=8385802;
RA   Lange-Carter C.A., Pleiman C.M., Gardner A.M., Blumer K.J.,
RA   Johnson G.L.;
RT   "A divergence in the MAP kinase regulatory network defined by MEK
RT   kinase and Raf.";
RL   Science 260:315-319(1993).
RN   [4]
RP   SEQUENCE OF 796-1493 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Heart;
RA   Whitmarsh A.J., Shore P., Sharrocks A.D., Davis R.J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE MAPKK 1 AND MAPKK 2
CC       (MEK1/MEK2) WHICH LEADS TO PHOSPHORYLATION OF MAP KINASES.
CC       POTENTLY ACTIVATES THE JNK/SAPK GROUP OF MAP KINASES.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HEART AND SPLEEN WHILE
CC       A LOWER LEVEL EXPRESSION IS SEEN IN THE LIVER.
CC   -!- PTM: AUTOPHOSPHORYLATED.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       MAP KINASE KINASE KINASE SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF117340; AAD25049.1; -.
DR   EMBL; AB014614; BAA85878.1; -.
DR   EMBL; L13103; AAA97500.1; ALT_INIT.
DR   EMBL; U23470; AAA85038.1; -.
DR   HSSP; Q00534; 1B17.
     MGD; MGI:1346872; Map3k1.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR   PROSITE; PS00089; ZF_RING_2; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Zinc-finger.
FT   DOMAIN        1224   1489       PROTEIN KINASE.
FT   ZN_FING        438    487       RING-TYPE.
FT   DOMAIN          25     32       POLY-GLY.
FT   DOMAIN          74    149       PRO-RICH.
FT   DOMAIN         233    291       PRO-RICH.
FT   DOMAIN         417    426       POLY-SER.
FT   NP_BIND       1230   1237       ATP (BY SIMILARITY).
FT   BINDING       1253   1253       ATP (BY SIMILARITY).
FT   ACT_SITE      1350   1350       BY SIMILARITY.
FT   CONFLICT        30     39       GGGALQGSGA -> ALQGSG (IN REF. 2).
FT   CONFLICT       103    103       MISSING (IN REF. 2).
FT   CONFLICT       257    257       V -> E (IN REF. 2).
FT   CONFLICT       307    307       M -> V (IN REF. 2).
FT   CONFLICT       413    413       S -> C (IN REF. 2).
FT   CONFLICT       559    559       V -> A (IN REF. 3).
FT   CONFLICT       883    883       V -> L (IN REF. 3).
FT   CONFLICT      1467   1467       V -> L (IN REF. 3).
SQ   SEQUENCE   1493 AA;  161288 MW;  CA65C9B7703C6BF9 CRC64;

Query Match                      88.4%;  Score 6920.5;  DB 1;  Length 1493;
Best Local Similarity   89.6%;  Pred. No. 1.1e-283;
Matches 1360;  Conservative  46;  Mismatches  81;  Indels  31;  Gaps  11;

Qy      1 MAAAAGNRASSGGPPGARATSPEA---GGGGALKASSAPAA-AAGLLREAGSGRERAD 56
          |||||| ||||| |||||||||| |||  |||| ||||||| ||||||| ||||||
Db      1 MAAAAGDRASSGFPGAAAASPEAGGGGGGALQGSGAPAAGAGLLREPGSAGRERAD 60

Qy     57 WRRRQLRKVRSVELDQLPEQPLFL-AASPPASSTSPSPEPADAAGSGTQPVAVPPPHG 115
          |||||||||||||||||||||||| |||| || ||||| | ||| ||| || || |
Db     61 WRRRQLRKVRSVELDQLPEQPLFLAAAASPPCPSTSPSPEPADAAAGASRFQPAAGPPPPG 120

Qy    116 AASRGAHLTESVAAPDSGASSPAAAEPGEKRAPAAEPSPAAAPAGREMENKETLKGLHK 175
          |||| |  |||  |||| ||||||||||| |||| ||||    | |||||||||||||
Db    121 AASRGGSHSAELAAAARDSGARSPAGAEP--------PS-AAAPSGREMENKETLKGLHK 170

Qy    176 MDDRPEERMIREKLKATCMPAWKHEWLERRNRRGPVVVKPIPVKGDGSEMNHLAAESPGE 235
          | |||||||||||||||||||||||||||||||||||||| || || || |||| |||
Db    171 MEDRPEERMIREKLKATCMPAWKHEWLERRNRRGPVVVKPIPIKGDGSEVNNLAAEPQGE 230

Qy    236 VQASAASPASKGRRSPSPGNSPSGRTVKSESPGVRRKRVSPVPFQSGRITPPRRAPSPDG 295
          ||  ||  |||||||||||| |||  ||| ||| |||||||||||||| ||||||||||
Db    231 GQAGSAAPAPKGRRSPSPGSSPSGRSVKPESPGVRRKRVSPVPFQSGRITPPRRAPSPDG 290

Qy    296 FSPYSPEETNRRVNKVMRARLYLLQQIGPNSFLIGGDSPDNKYRVFIGPQNCSCARGTFC 355
          ||||||||:|||||||||||||||||||||||||||||||||||||||||| |||| |||
Db    291 FSPYSPEETSRRVNKVMRARLYLLQQIGPNSFLIGGDSPDNKYRVFIGPQNCSCGRGAFC 350

Qy    356 IHLLFVMLRVFQLEPSDPMLWRKTLKNFEVESLFQKYHSRRSSRIKAPSRNTIQKFVSRM 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    351 IHLLFVMLRVFQLEPSDPMLWRKTLKNFEVESLFQKYHSRRSSRIKAPSRNTIQKFVSRM 410

Qy    416 SNSHTLSSSSTSTSSSENSIKDEEEQMCPICLLGMLDEESLTVCEDGCRNKLHHCMSIW 475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    411 SNSHTLSSSSTSTSSSENSIKDEEEQMCPICLLGMLDEESLTVCEDGCRNKLHHCMSIW 470

Qy    476 AEECRRNREPLICPLCRSKWRSHDFYSHELSSPVDSPSSLRAAQQOTVQQOPLAGS-RRN 534
          |||||||||||||||||||||||||||||||||| |||| | ||||| |||||| |||
Db    471 AEECRRNREPLICPLCRSKWRSHDFYSHELSSPVESPASLRAVQQPSSPQQPVAGSQRRN 530

Qy    535 QESNFNLTHYGTQQIPPAYKDLAEPWIQVFQMELVGCLFSRNWNVREMALRRLSHDVSGA 594
          ||| ||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    531 QESSFNLTHFGTQQIPSAYKDLAEPWIQVFQMELVGCLFSRNWNVREMALRRLSHDVSGA 590

Qy    595 LLLANGESTGNSGGSSGSSPSGGATSGSSQTSIGDVVEACCSVLSMVCADPVYKYVAA 654
          |||||||||||| ||| | |||  |||||| ||||||||||||| |||||||||||||
Db    591 LLLANGESTGNSGGGSGGSLSAGAASGSSQPSIGDVVEACCSVLSIVCADPVYKYVAA 650

Qy    655 LKTLRAMLVYTPCHSLAERIKLQRLLQPVVDTILVKCADANSRTSQLSISTLLELCKGQA 714
          |||||||||||||||||||||||||| |||||||||||||||||||||||| |||||||
Db    651 LKTLRAMLVYTPCHSLAERIKLQRLLRPVVDTILVKCADANSRTSQLSISTVLELCKGQA 710

Qy    715 GELAVGREILKAGSIGIGGVDYVLNCILGNQTESNNWQELLGRLCLIDRLLLEFPABFYP 774
          |||||||||||||||| ||||||| |||||| ||||||||||||||||||||||||||||
Db    711 GELAVGREILKAGSIGVGGVDYVLSCILGNQAESNNWQELLGRLCLIDRLLLEFPABFYP 770

Qy    775 HIVSTDVSQAEPVEIRYKKLLSLLTFALQSIDNSHSMVGKLSRRIYLSSARMVTTVPHVF 834
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    771 HIVSTDVSQAEPVEIRYKKLLSLLTFALQSIDNSHSMVGKLSRRIYLSSARMVTAVPAVF 830

Qy    835 SKILEMLSVSSSTHFTRMRRRLMAIADEVEIAEAIQLGVEDTLDGQQDSFLQASVPNNYL 894
          ||  ||| |||||||||||||||||||||||||| |||||||||||||| ||  | | |
Db    831 SKLVTMLNASGSTHFTRMRRRLMAIADEVEIAEVIQLGVEDTVDGHQDS-LQAVAFTSCL 889

Qy    895 ETTENSSPECTVHLEKTGKGLCATKLSASSEDISERLASISVGPSSSTTTTTTEQPKP 954
          |||| | ||| || ||| |  |||||| ||  |||||| |   |  |||||||||| |
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Db    890  ---ENSSLEHTVHRKTGKGLSATRLSASSEDISDRLAGVSVGLPSS----TTTEQPXP  941
                |:|||||||||||||||| |:||||| | |:||| |||||||||||      |:|||
Qy    955  MVQTKGRPHSQCLNSSPLSHHSQLMFPALSTPSSSTPSVPAGTATDVSKHRLQGFIPCRI 1014
                 ||||||||||||||| |:||||| | |:||||  |||| |||      |:|||:|
Db    942  AVQTKGRPHSQCLNSSPLS-HAQLMFPAPSAPCSSAPSVP-----DISKHRPQAFVPCKI  995

Qy   1015  PSASPQTQRKFSLQFHRNCPENKDSDKLSPVFTQSRPLPSSNIHRPKPSSRPTPGNTSKQG 1074
           ||||||||||||||| |||| |:||||||||||||| ||||||||||||||||| |:|:|
Db    996  PSASPQTQRKFSLQFQRNCSEHRDSDQLSPVFTQSRPPPSSNIHRPKPSSRPVPGSTSKLG 1055

Qy   1075  DPSKNSMTLDLNSSSKCDDSFGCSSNSSNAVIPSDETVFTPVEEKCRLDVNTELNSSIED 1134
           : :|:||||||.:|: |||||||  .|.||||||||||||||||:|||||||||||||||
Db   1056  DATKSSMTLDLGSASRCDDSFGGGGNSGNAVIPSDETVFTPVEDKCRLDVNTELNSSIED 1115

Qy   1135  LLEEASMPSSDTTVTFKSEVAVLSPEKAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMA 1194
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1116  LLEEASMPSSDTTVTFKSEVAVLSPEKAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMA 1175

Qy   1195  MSASQDALPIVPQLQVENGEDIIIQQDTPETLPGHTKAKQPYREDTEWLKGQQIGLGAF 1254
           ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   1176  MSASQDALPIVPQLQVENGEDIIIQQDTPETLPGHTKAKQPYREDAEWLKGQQIGLGAF 1235

Qy   1255  SSCYQAQDVGTGTLMAVKQVTYVRNTSSEQEEVVEALREEIRMMSHLNHPNIIRMLGATC 1314
           |||||||||||||||||||||||||||||||| |||||||||||:|||||||||||||||
Db   1236  SSCYQAQDVGTGTLMAVKQVTYVRNTSSEQEVVEALREEIRMMGHLNHPNIIRMLGATC 1295

Qy   1315  EKSNYNLFIEWMAGGSVAHLLSKYGAFKESVVINTEQLLRGLSYLHENQIIHRDVKGAN 1374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1296  EKSNYNLFIEWMAGGSVAHLLSKYGAFKESVVINTEQLLRGLSYLHENQIIHRDVKGAN 1355

Qy   1375  LLIDSTGQRLRIADFGAAARLASKGTGAGEFQGQLLGTIAFMAPEVLRGQOYGRSCDVWS 1434
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1356  LLIDSTGQRLRIADFGAAARLASKGTGAGEFQGQLLGTIAFMAPEVLRGQOYGRSCDVWS 1415

Qy   1435  VGCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPGLRDVALRCLELQPQ 1494
           ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db   1416  VGCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPGLRDVAVRCLELQPQ 1475

Qy   1495  DRPPSRELLKHPVFRRTTW 1512
           |||||||||||||||||||
Db   1476  DRPPSRELLKHPVFRRTTW 1493
```

RESULT 3
M3K1_RAT
ID   M3K1_RAT   STANDARD;   PRT;   1493 AA.
AC   Q62925;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.1.-)
DE   (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1).
GN   MAP3K1 OR MEKK1 OR MEKK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS.
RC   TISSUE=Brain;
RX   MEDLINE=96224276; PubMed=8643568;
RA   Xu S., Robbins D.J., Christerson L.B., English J.M.,
RA   Vanderbilt C.A., Cobb M.H.;
RT   "Cloning of rat MEK kinase 1 cDNA reveals an endogenous membrane-
RT   associated 195-kDa protein with a large regulatory domain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:5291-5295(1996).
CC   -!- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE MAPKK 1 AND MAPKK 2
CC   (MEK1/MEK2) WHICH LEADS TO PHOSPHORYLATION OF MAP KINASES. MOST
CC   POTENTLY ACTIVATES THE JNK/SAPK GROUP OF MAP KINASES, AND LESS
CC   EFFICIENTLY ERK2 OR P38.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED.
CC   -!- TISSUE SPECIFICITY: MOST HIGHLY EXPRESSED IN SPLEEN, KIDNEY, AND
CC   LUNG.
CC   -!- PTM: AUTOPHOSPHORYLATED.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- MAP KINASE KINASE KINASE SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC   --
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; U48596; AAC52596.1; -.
DR   HSSP; Q00534; 1BI7.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser-thr_pkinase.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00518; 2F_RING_1; FALSE_NEG.
DR   PROSITE; PS50089; 2F_RING_2; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Zinc-finger.
FT   ZN_FING   433   482   RING-TYPE.
FT   DOMAIN   1224   1489   PROTEIN KINASE.
FT   DOMAIN   25   29   POLY-GLY.
FT   DOMAIN   74   149   PRO-RICH.
FT   DOMAIN   233   291   PRO-RICH.
FT   DOMAIN   412   421   POLY-SER.
FT   DOMAIN   1163   1168   POLY-GLU.
FT   NP_BIND   1230   1237   ATP (BY SIMILARITY).
FT   BINDING   1253   1253   ATP (BY SIMILARITY).
FT   ACT_SITE   1350   1350   BY SIMILARITY.
FT   MUTAGEN   1369   1369   D->A: INACTIVATION.
SQ   SEQUENCE 1493 AA; 161315 MW; 8C5F29F866898524 CRC64;

Query Match
Best Local Similarity 88.1%;   Score 6892.5; DB 1; Length 1493; Pred. No.1.7e-282;
Matches 1350; Conservative 45; Mismatches 96; Indels 23; Gaps 8;

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Qy     1  MAAAAGNRASSSGFPGARATSPEAGGGGALKASSAPAAAAGLLREAGSGGRERADWRRR  60
          |||||| |||||||||| ||||||||||||| ||| | ||||||||| |||||||||||
Db     1  MAAAAGDRASSSGFPGAAAASPEAGGGGALQGSGAPAAGAGLLRETGSAGRERADWRRQ  60

Qy    61  QLRKVRSVELDQLPEQPLFLAASPASSTSPSPEPADAAGSGTGFQPVAVPPHGAASRG 120
          ||||||||||||||||||||| ||| ||||||||||||  |:|||||    |||||||
Db    61  QLRKVRSVELDQLPEQPLFLTASPPCPSTSPSPEPADAAAGASGFQPAAAGPPPPGAASRC 120

Qy   121  GAHLTESVAAPDSGASSPAAAEPGEKRAPAAEPSPAAAPAGREMENKETLKGLHKMDDRP 180
          |:| :| .|| |||| ||  |||          |:-|||| |||||||||||||||||||
Db   121  GSHSAELAAARDSGARSPAGAEP---------PS-AAAPSGREMENKETLKGLHKMDDRP 170

Qy   181  EERMIREKLKATCMPAWKHEWLERRNRRGPVVVKPIPVKGDGSEMNHLAAESPGEVQASA 240
          ||||||||||||||||||||||||||||||||||||||:|||||||:|||| ||| ||:
Db   171  EERMIREKLKATCMPAWKHEWLERRNRRGPVVVKPIPIKGDGSEMNLAAELQGEQOAGS 230

Qy   241  ASPASKGRRSPSPGNSPSGRTVKSESPGVRRKRVSPVPFQSGRITPPRRAPSPDGFSPYS 300
          | ||.||||||||| ||.||: |.|||||||||||||||||||||||||||||||||||
Db   231  AAPAPKGRRSPSPGSSPGRSGKPESPGVRRKRVSPVPFQSGRITPPRRAPSPDGFSPYS 290

Qy   301  PEETNRRVNKVMRARLYLLQQIGPNSPLIGGDSPDNKYRVFIGPQNCSCARGTFCIHLLF 360
          ||||.|||||||||||||||||||||||||||||||||||||||||||||.|||||||||
Db   291  PEETSRRVNKVMRARLYLLQQIGPNSPLIGGDSPDNKYRVFIGPQNCSCGRGTFCIHLLF 350

Qy   361  VMLRVFQLEPSDPMLWRKTLKNFEVESLFQKYHSRSSRIKAPSRNTIQKFVSRMSNSHT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||.||
Db   351  VMLRVFQLEPSDPMLWRKTLKNFEVESLFQKYHSRSSRIKAPSRNTIQKFVSRMSNCHT 410
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us-09-697-898-2.rsp

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Qy  1499 SRELLKHPVRTTW 1512
         |||||||||||||
Db  1480 SRELLKHPVRTTW 1493


RESULT 4
BCK1_YEAST
ID   BCK1_YEAST     STANDARD;      PRT;   1478 AA.
AC   Q01389; P32894;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Serine/threonine protein kinase BCK1/SLK1/SSP31 (EC 2.7.-.-).
GN   BCK1 OR SLK1 OR SSP31 OR LAS3 OR YJL095W OR JO906.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92186847; PubMed=1545797;
RA   Costigan C., Gehrung S., Snyder M.;
RT   "A synthetic lethal screen identifies SLK1, a novel protein kinase
RT   homolog implicated in yeast cell morphogenesis and cell growth.";
RL   Mol. Cell. Biol. 12:1162-1178(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92104496; PubMed=1840547;
RA   Irie K., Araki H., Oshima Y.;
RT   "A new protein kinase, SSP31, modulating the SMP3 gene-product
RT   involved in plasmid maintenance in Saccharomyces cerevisiae.";
RL   Gene 108:139-144(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EG123;
RX   MEDLINE=92107166; PubMed=1729597;
RA   Lee K.S., Levin D.E.;
RT   "Dominant mutations in a gene encoding a putative protein kinase
RT   (BCK1) bypass the requirement for a Saccharomyces cerevisiae protein
RT   kinase C homolog.";
RL   Mol. Cell. Biol. 12:172-182(1992).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C;
RX   MEDLINE=95176706; PubMed=7871887;
RA   Miosga T., Boles E., Schaaff-Gerstenschlaeger I., Schmitt S.,
RA   Zimmermann F.K.;
RT   "Sequence and function analysis of a 9.74 kb fragment of
RT   Saccharomyces cerevisiae chromosome X including the BCK1 gene.";
RL   Yeast 10:1481-1488(1994).
RN   [5]
RP   SEQUENCE OF 602-1104 FROM N.A.
RA   Cusick M.E.;
RL   Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN A SIGNAL
CC       TRANSDUCTION PATHWAY THAT PLAY A ROLE IN YEAST CELL MORPHOGENESIS
CC       AND CELL GROWTH. THIS PATHWAY SEEMS TO STARTS BY SMP3; THEN
CC       INVOLVE THE KINASE PKC1 THAT MAY ACT ON THIS KINASE. BCK1 PROBABLY
CC       PHOSPHORYLATES MKK1 AND MKK2 WHICH THEMSELVES PHOSPHORYLATE THE
CC       MPK1 KINASE.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       MAP KINASE KINASE KINASE SUBFAMILY.
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; M84389; -; NOT_ANNOTATED_CDS.
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Qy   421 LSSSTSTSSSENSIKDEEEQMCPICLLGMLDEESLTVCEDGCRNKLHHCMSIWAEECR 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   411 LSSSTSTSSSENSIKDEEEQMCPICLLGMLDEESLTVCEDGCRNKLHHCMSIWAEECR 470

Qy   481 RNREPLICPLCRSKWRSHDFYSHELSSPVDSPSSLRAAQQOTVQQOPLAGS-RRNQESNF 539
         ||||||||||||||||||||||||||||||||  ::  ||  :|| |||  ||||||||
Db   471 RNREPLICPLCRSKWRSHDFYSHELSSPVDSPTSLRGVQQPSSPQOPVAGSQRRNQESNF 530

Qy   540 NLTHYGTQQIPPAYKDLAEPWIQVFGMELVGCLFSRNWNVREMALRRLSHDVSGALLLAN 599
         |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db   531 NLTHYGTQQIPPAYKDLAEPWIQAFGMELVGCLFSRNWNVREMALRRLSHDVSGALLLAN 590

Qy   600 GESTGNSGGSGSGSSPSGGATSGSSQTSISGDVVEACCSVLSMVCADPVYKVYVAALKTLR 659
         |||||.|||.|..|| |:|:||||||.||||||||| |||||:||||||||.|||||||||
Db   591 GESTGISGGGSGGGSLSAGAASGSSQPSISGDVVEAFCSVLSIVCADPVYKYYVAALKTLR 650

Qy   660 AMLVYTPCHSLAERIKIQRLLQPVVDTILVKCADANSRTSQLSISTLLELCKGQAGELAV 719
         |||||||||||||||:|||| ||||||||||||||||||||||||||||||||||||||||
Db   651 AMLVYTPCHSLAERIKLQRLLRPVVDTILVKCADANSRTSQLSISTLLELCKGQAGELAV 710

Qy   720 GREILKAGSIGIGGVDYVLNCILGNQTESNNWQELLGRLCLIDRLLLEFPAEFYPHIVST 779
         ||||||||||.||||||||.||||||.|||||||||||||||||||||  ||||||||||
Db   711 GREILKAGSIGVGGVDYVLSCILGNQAESNNWQELLGRLCLIDRLLLEISAEFYPHIVST 770

Qy   780 DVSQAEPVEIRYKKLLSLLTFALQSIDNSHSMVGKLSRRIYLSSARMVTTVPHVFSKLLE 839
         ||||||||||||||||||||.||||||||||||||||||||||||||||||:.|||||::
Db   771 DVSQAEPVEIRYKKLLSLLAFALQSIDNSHSMVGKLSRRIYLSSARMVTTVPPLFSKLVT 830

Qy   840 MLSVSSSTHFTMRRRLMAIADEVEIAEAIQLGVEDTLDGQQDSFIQASVPNNYLETTEN 899
         |||.:.:|||..||||||||||||||| ||||.|||||||||     |  | :   |:|
Db   831 MLSASGSSHFARMRRRLMAIADEVEIAEVIQLGSEDTLDGQQDS-SQALAPPRY---PES 886

Qy   900 SSPECTVHLEKTGKGLCATKLSASSEDISERLASISVG-PSSSTTTTTTTEQPKPMVQT 958
         ||  .|.|:|||||||.||:|||||||||.|||.:|||  :|||       |||||:|||
Db   887 SSLEHTAHVEKTGKGLKATRLSASSEDISDRLAGVSVGLPSSA------TTEQPKPTVQT 940

Qy   959 KGRPHSQCLNSSPLSHSQLMPPALSTPSSSTPSVPAGTATDVSKIRLQGFIPCRIPSAS 1018
         |||||||||||||||  |||||||:|  ||:||||||..|||||||  ||:||.|||||
Db   941 KGRPHSQCLNSSPLS-PPQLMPPAISAPCSSAPSVPAGSVTDASKHRPRAFVPCKIPSAS 999

Qy  1019 PQTQRKFSLQFHRNCPENKDSDKLSPVFTQSRPLPSSNIHRPKPSRPTPGNTSKQGDPSK 1078
         |||||||||||.|.| ||.||||||||||.| .|||||||||.||.|||| |||||.|:|
Db  1000 PQTQRKFSLQFQRTCSENRDSEKLSPVFTQSPRPPSSNIHRAKASRPVPGSTSKLGDASK 1059

Qy  1079 NSMTLDLNSSSKCDDSFGCSSNSSNAVIPSDETVFTPVEEKCRLDVNTELNSSIEDLLEA 1138
         ||||||||:::|||||||.:.|:.:||||||||.|||.|:|||||||.||||||||||||
Db  1060 NSMTLDLNSASQCDDSFGSGSNSGSAVIPSEETAFTPAEDKCRLDVNPELNSSIEDLLEA 1119

Qy  1139 SMPSSDTTVTFKSEVAVLSPEKAENDDTYKDDVNHNQCKCEKMEAEEEEALAIAMAMSAS 1198
         |||||||||||||||||||||||||.||||||||||||.|||||||||||||||||||||
Db  1120 SMPSSDTTVTFKSEVAVLSPEKAESDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSAS 1179

Qy  1199 QDALPIVPQLQVENGEDIIIIQQDTPETLPGHTKAKQPYREDTEWLKGQQIGLGAFSSGY 1258
         ||||||||||||||||||||||||||||||||||| :|||||||||||||||||||||.|
Db  1180 QDALPIVPQLQVENGEDIIIIQQDTPETLPGHTKANEPYREDTEWLKGQQIGLGAFSSCY 1239

Qy  1259 QAQDVGTGTLMAVKQVTVRNTSSEQEEVVEALREEIRMMSHLNHPNIIRMLGATCEKSN 1318
         |||||||||||||||||.||||||||||||||||||||||||||||||||||||||||
Db  1240 QAQDVGTGTLMAVKQVTYVRNTSSEQEEVVEALREEIRMMSHLNHPNIIRMLGATCEKSN 1299

Qy  1319 YNLFIEWMAGGSVAHLLSKYGAFKESVVINTEQLLRGLSYLHENQIIHRDVKGANLLID 1378
         |||||||||..|||||||||||||||||||||||||||||||||||||||||||||||
Db  1300 YNLFIEWMAGASVAHLLSKYGAFKESVVINTEQLLRGLSYLHENQIIHRDVKGANLLID 1359

Qy  1379 STGQRLRIADFGAAARLASKGTCAGEFQGQLLGTIAPMAPEVLRGQYGRSCDVWSVGCA 1438
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1360 STGQRLRIADFGAAARLASKGTCAGEFQGQLLGTIAPMAPEVLRGQYGRSCDVWSVGCA 1419

Qy  1439 IIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPGLRDVALRCLELQPQDRPP 1498
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1420 IIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPGLRDVALRCLELQPQDRPP 1479
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DR   EMBL; D10389; BAA01226.1; -.
DR   EMBL; X60227; CAA42788.1; -.
DR   EMBL; X77923; CAA54896.1; -.
DR   EMBL; Z49370; CAA89389.1; -.
DR   EMBL; Z49369; CAA89388.1; -.
DR   EMBL; M88604; AAA21179.1; -.
DR   PIR; S20117; S20117.
DR   PIR; S22285; S22285.
DR   PIR; JQ1118; JQ1118.
DR   PIR; JQ1432; JQ1432.
DR   HSSP; P24941; 1CKP.
DR   SGD; S0003631; BCK1.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; EuK_pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
KW   ATP-binding; Phosphorylation.
FT   DOMAIN    1175   1440   PROTEIN KINASE.
FT   NP_BIND   1181   1189   ATP (BY SIMILARITY).
FT   BINDING   1204   1204   ATP (BY SIMILARITY).
FT   ACT_SITE  1303   1303   BY SIMILARITY.
FT   MOD_RES   1134   1134   PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   VARIANT   1119   1119   T -> P (IN BCK1-19; ACTIVATION).
FT   VARIANT   1120   1120   I -> K (IN BCK1-11; ACTIVATION).
FT   VARIANT   1120   1120   I -> T (IN BCK1-16; ACTIVATION).
FT   VARIANT   1146   1146   G -> V (IN BCK1-10; ACTIVATION).
FT   VARIANT   1174   1174   A -> P (IN BCK1-20; ACTIVATION).
FT   CONFLICT    59     59   F -> I (IN REF. 3).
FT   CONFLICT    79     79   E -> V (IN REF. 2).
FT   CONFLICT   264    264   A -> P (IN REF. 3).
FT   CONFLICT   279    279   N -> I (IN REF. 3).
FT   CONFLICT   703    714   RYQTPSYYYDR -> STPKPRVITMIE (IN REF. 3).
FT   CONFLICT   795    795   S -> A (IN REF. 3).
FT   CONFLICT   802    802   L -> V (IN REF. 3).
FT   CONFLICT   808    808   A -> S (IN REF. 3).
FT   CONFLICT   903    903   T -> N (IN REF. 3).
FT   CONFLICT   919    919   T -> N (IN REF. 3).
FT   CONFLICT   960    962   ADA -> RDR (IN REF. 5).
FT   CONFLICT  1086   1104   RPVPPDSSYEFIQDGLNGK -> VPIAHTSSYRMDLTVKIN
FT                           H (IN REF. 5).
SQ   SEQUENCE  1478 AA;  164194 MW;  D586C3A497A5BB33 CRC64;

Query Match             7.9%;  Score 619;  DB 1;  Length 1478;
Best Local Similarity  21.08%;  Pred. No. 5.2e-19;
Matches 332;  Conservative 232;  Mismatches 552;  Indels 466;  Gaps 64;

Qy   224  EMNHLAAESPGEVQASAASPASKGR------RSPSPG--NSPSGRTVKSESPGVRRKR  273
Db    24  KFGHQPTSSVASTKSSSKSPRATSRKSIYDDIRSQFPNLIPNSTSSQFYES-------  74

Qy   274  VSPVPFQSGRITPPRRAPSPDGFSPYSPEETNRRVNKVMRARLYLLQQIGPNSFLIGGDS  333
Db    75  -TPVIEQSFNWT------TDDHISAGTLE-------------------NPTSFTNSSYK  107

Qy   334  PDNKYRVFIGPQNCSCAR--GTFCIHLLFVMLRVFQLEPSDPMLW---RKT-------  379
Db   108  NDN------GPSSLSDSRKSSGGNSVNSLSFDKLILSWDPTDPDEWTMHRVISWFKFHDF  161

Qy   380  ------------LKNFEVESLFQKYHSRRSSRIKAPSRNTIQKFVSR-MSNS  418
Db   162  PESWILFFKKHQLFGHRFIKLLAVDNFAVYEKYLPQTKTASYTRFQQLLKKTMTKNVTNS  221

Qy   419  H-------TLSSSSTPSTSSSENSIKDEEEQMCPICLLGMLDEESLTVCEDGC----RNK  466
Db   222  HIRQKSASIKLKSSRSSSSESIKSKLKNSKSQE-DISNSRSTSESALSPTKSGPSKTDEKNF  280

Qy   467  LHHHCMSIWAEECRNREPLICPLCRSKWRSHDFYSHELSSPVDSPSSLRAAQQQTVQQQ  526
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Db   281  LH-------STSTHQKTKSASSLYRRSFISLRGSSSNASSAKSPSNIKL----SIPAR  328
Qy   527  PLAGSRRNQESNFNLTHYGTQQIPPAYKDLAEPWIQVFGMELVGCLFSRNWNVREMALRR  586
Db   329  P---HSIIESNSLTKSASPPASPSYPS-----------------IFRRH-------HK  360
Db   587  LSHDVSGALLANGESTGNSGGSGSSSPSGGATSGSS-----------QTSISGDVVEACCS  637
Db   361  SSSSESSLLNSLFGSGIGEEAPTK-PNPQGHSLSSENLAKGKSKHYETNVSSPLKQS---  416
Qy   638  VLSMVCADPVYKVYVAALKTLRAMLVYTPCHSLAERIKLQRLLQPVPVDTILVKCADANSR  697
Db   417  --SLPTSDDKGNLW--NKFKRKSQIGVFSPNTVAYVTSQ---EIPSLK---SNSS  461
Qy   698  TSQLSISTL---LELCKGQAGELAVGREILKAGSIGIGGVDYVLNCILGN  744
Db   462  TATLTVQTADVNIPSPSSPPIPKTANRSLEVISTEDTPKISSTTASFKETYPDCINPD  521
Qy   745  QT--ESNNWQELLGRLCLIDRLLEFPAEFYPHIVSTDVSQAE-----------PV  787
Db   522  KTVPVPVNN-QKYSVKNFLDDQ------KFYP-LKKTGLNDSENKYILVTKDNVSFVPL  572
Qy   788  EIR-YKKLLSLLTFALQSIDNSHSMV--------------------------GK  814
Db   573  NLKSVAKLSSFKESALTKLGINHKNVTFHMTDFDCDIGAAIPDDTLEFLKKSLFLNTSGK  632
Qy   815  LSRRIYLSSARMVTTVPHVFSKLLEMLSVSSSTHFTMRRRLMAIADEVEIAEAIQ--LG  872
Db   633  IYIKDQMKLQQKPKAPLTSENNVPLKSVKSKSSMRSGTSSLIASTDDVSIVTSSSDITS  692
Qy   873  VEDTLDGQQDSFLQASVPNNYLETTENSSP-----------ECTVHLEKTGKGLCAT--KL  920
Db   693  FDEHASGSGRRYPQ--TPSYYYDRVSNTNPTEELNYWNIKEVLSHEENAPKMVFKTSPKL  750
Qy   921  SASSEDISERLASISVGPSSSTTTTTTTEQKPKPMVQTKGRPHSQCLNSS----PLSHH  975
Db   751  ELNLPDKGSKL---------------NIPTPITENESKSSFQVLRKDEGTEIDFNHR  792
Db   976  SQLMF-PALSTPSSSTPSVPAGTATDVSKHRLQGFIPCRIPSASPQTQRKFSLQFHRNC  1033
Db   793  RESPYIKPELA-PKREAPKPANTSQRTLSTSKQNKPIRLVRASTKISRS----------  842
Qy  1034  PENKDSDKLSPVFTQSRPLPSSNIHRP-KPSRPTPGNTSKQGDPSKNSMTL--------D  1084
Db   843  ------KRSKPLPQLLSSPIEASSSSPDSLTSSYTPASTHVLIPQPYKGAND  889
Qy  1085  LNSSSKCD-DSFGCSS-----------------NSSNAVIPSDETVF--TP----VEEKCRL  1122
Db   890  VMRRLKTDQDSTSTSPSLKMQKQVNRSNSTVSTSNSIFYSPSPLLKRGNSRKRVVSSTSAA  949
Qy  1123  DVNTELNSSIEDLLEASMP--------------SSDTTVTFKSEVAV-----LSPEKAEN  1163
Db   950  DIFEE----NDITFADAPPMFDSDDSDDDSSSSDDIIWSKKKTAPETNNENKKDEKSDN  1004
Qy  1164  DDTYKDDVNHNQKCKEKME-------------AEEEEALAIAMAMSASQDA  1201
Db  1005  SSTHSDEIFYDSQTQDKMERKMTFRPSPEVVYQNLEKFFPRANLDKPITEGIASPTSPKS  1064
Qy  1202  L----------------PIVPQLQVE----NGEDIIIQQDTP------  1224
Db  1065  LDSLLSPKNVASSRTEPSTPSRPVPPDSSYEFIQDGLNGKNKPLNQAKTPKRTKTIRTIA  1124
Qy  1225  ----------------ETLPGH---TKAKQPYREDTE--WLKGQQIGLG  1252
Db  1125  HEASLARKNSVLKRQNTKMWGTRMVEVTENHMVSINKAKNSKGEYKFAWMKGEMIGKG  1184
Qy  1253  AFSSCYQAQDVGTGTLMAVKQVTYVRNTSSEQEV----VEALREIRMMSHLNHPNIIRM  1309
Db  1185  SFGAVYLCLNVTTGEMMAVKQVE-VPKYSSQNEAILSTVEALRSEVSTLKDLLHLNIVQY  1243
Qy  1310  LGATCEKSNYNLPIEWMAGGSVAHLLSKYGAFKESVVINYTEQLLRGLLSYLHENQIIHRD  1369
Db  1244  LGFENKNNIYSLPEYVAGGSVGSLIRMYGRFDEPLIKHLTTQVLKGLAYLHSKGLIHRD  1303
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Db    110 SSSMKSLRILLSQDRN--HTSSSPHSGVSRQVRIKPSQSAGDINTIYQAPEPRSRHLS 166
Qy   1063 ------SRPTPG------NTSKQGDPSKNSMTLDLNSSSKCDDSFGCSSNSSNAVIP 1107
                 :|:|          |:   |:: :  |:       ||
Db    167 VSSQNPGRSSPPPGYVPERQQHIARQG----SYT-----------SINSEGEFIP 206
                  :|:     | |                 |
Qy   1108 SDETVFTPVEEKCRLDVNTELNSSIEDLLEASMPSSDTTVTFKSEVAVLSP--------- 1158
           | :|    ||::|: |::  :|:|| |:::
Db    207 E------TSEQCMLDPLSSAENSLSGSCQSLDRSADSPSFRKSQMSRARSFPDNRKECS 259
            :         ::||:  || | :   ::::|
Qy   1159 -----EKAENDDTY---------KDDVNHNQKCKEKMEAEEEEALAI--AMAMSASQ 1199
                |::||:||          ||:|:| |:||:|| : :::  :::::
Db    260 DRETQLYDKGVKGGTYPRRYHVSVHHKDYNDGRRTFPRIRRHQGNLFTLVPSSRSLSTNG 319
             ::|   |:
Qy   1200 DALPIVPQ-------LQVENGEDIIIQQDTPETLPGHTKAKQPYREDTEWLKGQQIGLG 1252
           ::|::          |: : :  :: ::|  |   |||   :|::    |||:|||:|||
Db    320 ENMGVAVQYLDPGRGRLRSADSENALTVQERRVPT-------KSP-SAPINWRRGKLLGQG 371
Qy   1253 AFSSCYQAQDVGTGTLMAVKQVTYVRNTSSEQEEVVEALREEIRMMSHLNHPNIIRMLGA 1312
           || |  |  ::| |  :|: ||:| |  : |  | ||  |||  || :||:|||:| | |
Db    372 AFGRVLVCYDVDTGRELASKQVQFPDD-SPETSKEVSALECEIQLLKNLQHERIVQYYGC 430
Qy   1313 TCEKSN--YNLFIEWMAGGSVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIHRDV 1370
               ::|  ::|:|:||| ||| |||    | |  :|:  : |::|||||||:|:|:|||:
Db    431 LRDRAEKILTIFMEYMPGGSVKDQLKAYGALTESVTRKYTRQILEGMSYLHSNMIVHRDI 490
Qy   1371 KGANLLIDSTGQRLRIADFGAAARLAS--KGTGAGEFQGQLLGTIAFMAPEVLRGQQYG 1427
           ||||:| ||:| :|: :||||:  ||:   |||:|||:|:|||||:||||||  |::|
Db    491 KGANILRDSAG-NVKLGDFGASKRLQTICMSGTGI----RSVTGTPYWMSPEVISGEGYG 545
Qy   1428 RSCDVWSVGCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPGLRDVALR 1487
           | ||||| || :|||  :|||| ||   : || |||||:|  ||:|||| |  |:  :|
Db    546 RKADVWSLGCTVVEMLTEKPPW-AEYEA-MAAIFKIATQPTNPQLPSHISEHGRDF-LR 601
Qy   1488 CLELQPQDRPPSRELLKH 1505
           | :: :| ||| :|||:|
Db    602 RIFVEARQRPSAEELLTH 619

RESULT 6
M3K3_HUMAN
ID   M3K3_HUMAN     STANDARD;      PRT;   626 AA.
AC   Q99759;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Mitogen-activated protein kinase kinase kinase 3 (EC 2.7.1.-)
DE   (MAPK/ERK kinase kinase 3) (MEK kinase 3) (MEK 3).
GN   MAP3K3 OR MAPKKK3 OR MEKK3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97165568; PubMed=9006902;
RA   Ellinger-Ziegelbauer H.C., Brown K., Kelly K., Siebenlist U.;
RT   "Direct activation of the stress-activated protein kinase (SAPK) and
RT   extracellular signal-regulated protein kinase (ERK) pathways by an
RT   inducible mitogen-activated protein Kinase/ERK kinase kinase 3 (MEKK)
RT   derivative.";
RL   J. Biol. Chem. 272:2668-2674(1997).
CC   -!- FUNCTION: PREFERENTIALLY ACTIVATES P42/44 (ERK2/ERK1) MAP KINASES.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       MAP KINASE KINASE KINASE SUBFAMILY.
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Qy   1370 VKGANLLIDSTGQRLRIADFGAAARLASKGTGAGEFQGQLLGTIAFMAPEVLRQQQ-YGR 1428
           :| ||:|| ||:| :|: |||||:  ||:  : |:::    | | :::| ||::  :|
Db   1304 MKADNLLLDQDG-ICKISDFGISRK-SKDIYSNS-DMTMRGTVFWMAPEVDTKQGYSA 1359
Qy   1429 SCDVWSVGCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPGLRDVALR- 1487
           | |:||:|| ::|| | |||||   |  : :::||:: | || |||  |: :| |||:
Db   1360 KVDIWSLGCIVLEMFAGKRPWS---NLEVVAAMFKIGKSKSAPPIPEDTLPLISQIGRNF 1416
Qy   1488 --CLELQPQDRPPSRELLKHP 1506
             : | :||::||| ||||:|
Db   1417 LDACFEINPEKRPTANELLSHP 1438

RESULT 5
M3K3_MOUSE
ID   M3K3_MOUSE     STANDARD;      PRT;   626 AA.
AC   Q61084;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Mitogen-activated protein kinase kinase kinase 3 (EC 2.7.1.-)
DE   (MAPK/ERK kinase kinase 3) (MEK kinase 3) (MEKK 3).
GN   MAP3K3 OR MEKK3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96214986; PubMed=8621389;
RA   Blank J.L., Gerwins P., Elliott E.M., Sather S., Johnson G.L.;
RT   "Molecular cloning of mitogen-activated protein/ERK kinase kinases
RT   (MEKK) 2 and 3. Regulation of sequential phosphorylation pathways
RT   involving mitogen-activated protein kinase and c-Jun kinase.";
RL   J. Biol. Chem. 271:5361-5368(1996).
CC   -!- FUNCTION: PREFERENTIALLY ACTIVATES P42/44 (ERK2/ERK1) MAP KINASES.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       MAP KINASE KINASE KINASE SUBFAMILY.
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DR   EMBL; U43187; AAB03535.1; -.
DR   HSSP; Q00534; 1B1B.
DR   MGD; MGI:1346874; Map3k3.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding.
FT   DOMAIN      362    622       PROTEIN KINASE.
FT   NP_BIND     368    375       ATP (BY SIMILARITY).
FT   BINDING     391    391       ATP (BY SIMILARITY).
FT   ACT_SITE    489    489       BY SIMILARITY.
SQ   SEQUENCE   626 AA;  70775 MW;  00EF2442C9E56E0B CRC64;

Query Match            7.1%;  Score 559;  DB 1;  Length 626;
Best Local Similarity  29.9%;  Pred. No. 6.4e-17;
Matches  167;  Conservative   87;  Mismatches  188;  Indels  116;  Gaps   21;

Qy   1016 SASPQTQRKFSLQFHRNCPENKDSDKLSPVFTQSRPLPSSN-----IHRPKP------ 1062
           |:| :      :       :  |:|     | :|  | |::      :|||||
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CC
DR   EMBL; U78876; AAB41729.1; -.
DR   HSSP; Q00534; 1BI8.
DR   Genew; HGNC:6855; MAP3K3.
DR   MIM; 602539; -.
DR   InterPro; IPR000719; Euk_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00220; S_Tkc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding.
FT   DOMAIN      362    622    PROTEIN KINASE.
FT   NP_BIND     368    375    ATP (BY SIMILARITY).
FT   BINDING     391    391    ATP (BY SIMILARITY).
FT   ACT_SITE    489    489    BY SIMILARITY.
SQ   SEQUENCE   626 AA;   70969 MW;   E0F11F5082E9A810 CRC64;

Query Match             7.1%;
Best Local Similarity   30.3%;   Pred. No. 6.7e-17;
Matches  164;   Conservative  85;   Mismatches  191;   Indels  101;   Gaps  20;

Qy  1016  SASPQTQRKFSLQFHRNCPENKDSDKLSPVFTQSRPLPSSNIHRPKPSRPTPG------ 1068
                :::||         :     |  ::  |  || ::   |::  |        ||
Db   129  SSSPHSEVSRQVRIKASQSAGDINTIYQPEPRSRHLSVSS-QNPGRSSPPPGIYPERQQ  187

Qy  1069  NTSKQGDPSKNSMTLDLNSSSKCDDSFGCSSNSNAVIPSDETVFTPVEEKCRLDVNTEL 1128
                 :::||     |         |       ||      ||     :  |     ||
Db   188  HIARQG-----SYT-------------SINSEGGFIPE------TSEQCMLDP----   216

Qy  1129  NSSIEDLLEASMPSSDTTV--TFKSEVAVLSPEKAENDDTYKD---------------- 1169
              | :   : || |  :::  :|      |  :   |     |
Db   217  LSSAENSLSGSCQSLDRSADSPSFRKSRMSRAQSPFDNRQEYSDRETQLYDKGVXGGTYP  276

Qy  1170  --------DVNHNQCKEKMEAEEEEALAI--AMAMSASQDALPIVPQ-------LQ 1209
                            |:   |:|          :  |   | |         |:
Db   277  RRYHVSVHHKDYSDGRRTFPIRRHQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRLR  336

Qy  1210  VENGEDIIIQQDTPETLPGHTKAKQYREDTEWLKGQQIGLGAFSSCYQAQDVGTGTLM 1269
             :  ||         |     ||    |  |    |  |   ||   :     |  |
Db   337  SADSENALSVQERNVPT------KSP-SAPINWRRGKLLGQGAFGRVYLCYDVDTGREL  388

Qy  1270  AVKQVTVVRNTSSEQEVVEALREEIRMMSHLNHPNIIRMLGATCEKSNYNL--FIEWMA 1327
             ||   :|      :|       | | | ::  |: | :  ||     :  |  ::::
Db   389  ASKQVQFPDPD-SPETSKEVSALECEIQLLKNLQHERIVQYYGCLRDRAEKTLTIFMEYMP  447

Qy  1328  GGSVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIIHRDVKGANLLIDSTGQRLRIA 1387
             ||   |                  | |  |  | :  : |||  |:|  ::|       |
Db   448  GGSVKDQLKAYGALTESVTRKYTRQIIEGMSYLHSMVIHRDIKGANILRDSAG-NVKLG  506

Qy  1388  DFGAARLAS--KGTGAGEFGQGLLGTIAFMAPEVLRGQQYGRSCDVWSVGCAIIEMAC 1444
             ||  |  :  | | || ||      ||   : ||      :| : || || ||  |
Db   507  DFGASKRLQTICMSGTG---MRSVTGTPYWMSPEVISGEGYGRKADVWSLGCTVVEMLT  562

Qy  1445  AKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPGLRDVALRCLELQPQDRPPSRELLK 1504
             ::   |       |  | |:    |  |:: | :||   |  ::  |   ||  | |||
Db   563  EKPPW-AEYEA-MAAFKIATQPTNPQLPSHISEHGRDF-LRRIFVEARQRPSAEELLT  618

Qy  1505  H 1505
           |
Db   619  H 619

RESULT 7
BYR2_SCHPO
ID   BYR2_SCHPO     STANDARD;    PRT;    659 AA.
AC   P28829;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein kinase byr2 (EC 2.7.1.-) (Protein kinase ste8) (MAPK kinase
DE   kinase) (MAPKK).
GN   BYR2 OR STE8 OR SPBC1D7.05.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91260705; PubMed=2046669;
RA   Wang Y., Xu H.P., Riggs M., Rodgers L., Wigler M.;
RT   "byr2, a Schizosaccharomyces pombe gene encoding a protein kinase
RT   capable of partial suppression of the ras1 mutant phenotype.";
RL   Mol. Cell. Biol. 11:3554-3563(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93062799; PubMed=143572;
RA   Styrkarsdottir U., Egel R., Nielsen O.;
RT   "Functional conservation between Schizosaccharomyces pombe ste8 and
RT   saccharomyces cerevisiae STE11 protein kinases in yeast signal
RT   transduction.";
RL   Mol. Gen. Genet. 235:122-130(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   -!- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN CONJUGATION
CC       AND SPORULATION. IT IS THOUGHT THAT IT PHOSPHORYLATES THE BYR1
CC       PROTEIN KINASE WHICH ITSELF PHOSPHORYLATE THE SPK1 KINASE.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       MAP KINASE KINASE SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
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DR   EMBL; M74293; AAA35289.1; -.
DR   EMBL; X68851; CAA48731.1; -.
DR   EMBL; Z98270; CAB10981.1; -.
DR   PIR; A39723; A39723.
DR   PIR; S30094; S30094.
DR   HSSP; Q63450; 1A06.
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DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR001660; SAM.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00536; SAM; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00454; SAM; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50105; SAM_DOMAIN; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Conjugation; Sporulation.
FT   DOMAIN        4     67       SAM.
FT   DOMAIN      394    658       PROTEIN KINASE.
FT   NP_BIND     400    408       ATP (BY SIMILARITY).
FT   BINDING     423    423       ATP (BY SIMILARITY).
FT   ACT_SITE    522    522       BY SIMILARITY.
SQ   SEQUENCE    659 AA;  73632 MW;  1BCD78F1D1FABBCD CRC64;

Query Match             6.9%;  Score 543.5;  DB 1;  Length 659;
Best Local Similarity   26.28%;  Pred. No. 3e-16;
Matches  181;  Conservative  115;  Mismatches  259;  Indels  137;  Gaps  27;

Qy   871 LGVEDTLDGQDSFLQASVPNNYLETTENSSP-----EC--TVHLEKTG--KGLCAT 918
             ||:|:|| :|: |:     :||     :    |: ||      | |
Db    46 LGIENTAKGKQ-FLK--QRDYLR--EFPRPCILRFIACNGQTRAVQSRGDYQKTLAIA 98

Qy   919 KLSASSEDISERLASISVGPSSTTTTTTEQPKMVQTKGRPHSQCLNSSPLSHHSQL 978
             | ||:||:|::   |:||: | :::| ||||              |||
Db    99 LKKFSLEDASKFIVCV----SQSRKILITEEFKQI-------CFNSSSPERDRLI 144

Qy   979 MFP------------------ALSTPSSTPSVPAGTATDVSKHRLQGFIPCRIP 1015
             |||                  || |||| |||||||||||||||||||||||
Db   145 IVPKEKPCPSFEDLRRSWEIELAQPAALSSQSSLSPKLSSVLPTSTQKRSV---RSN 198

Qy  1016 SASPQTQRKFSLQFHRNCPENKDSDKLSPVFTQSRPLPSSNIHRPKPSRPTPGNTSKQGD 1075
             :|       |:    |:       |:||                  :::|:|
Db   199 NAKP------FESYQRPPSELINSRISDFFPD----------HQPKILEKTISNSLRRNL 242

Qy  1076 PSKNSMTLDLNSSSKCDDSFGCCSSNSSNAVIPSDETVFTPVEEKCRLDVNTELNSSI-ED 1134
             |                          ||
Db   243 SIRTSQGHNL-------------GNFGQEILPRSSRRARPSELVCPL--SSLRISVAED 286

Qy  1135 L--LEASMPSSDTTVTFKSEVAVLSPEKAENDDT------YKDDVNHNQKCKEKMEAEE 1185
                |:|:|       | : :| :    |:|| |      |:|
Db   287 VNRLPRIDRGFDPPLTVSSTQRISRPPSLQKSITMVGVEPLYQS--NGNEKSSKYNVFSE 344

Qy  1186 ------EEFALAIAMAMSAS--QDALPIVPQLQVENGEDIIIIQQDTPETLPGHTKAKQPYR 1238
                        |     |:| |           | ::||       ||:||
Db   345 SAHGNHQYLSFSPGSSPSFIEQSPISP--TSTTSEDTNTLEEDTDD------------ 389

Qy  1239 EDTEWLKGQQIGLGAFSSCYQAQDVGTGTLMAVKQVTY--VRNTSSQEEVVEALREIR 1296
             ||:| :  | || ||: ||| |  ||| | :| |      :||:|| : | |:||||
Db   390 QSIKWIRGALISGSFGQVYLGMNASSGELMAVKQVILDSVSESKDRHAKLLDALAGEIA 449

Qy  1297 MMSHLNHPNIIRMLGATCEKSNVNLFIEWMAGGSVAHLLSKYGAFKESVVINVTEQLLRG 1356
             |: | |||||  || | :|     ||||| ||| |  |||| ||: |:| ::|||:|||
Db   450 LIQELSHEHIVQYLGSNLNSDHLNIFLEYVPGGSVAGLLTMYGSFEETLVKNFIKQTLKG 509

Qy  1357 LSYLHENQIIHRDVKGANLLIDSTGQRLRIADFGAAARLA--SKGTGAGEFQGQLLGTIA 1414
             | |||  ||||| |||||| |  |:|||||||:|||     ||||  || ||  ||| |
Db   510 LEYIHSRGIVHRDIKGANLIVDNKG-KIKISDFGISKKLELNSTSTKTGGARPSFQGSSF 568

Qy  1415 FMAPEVLRGQQYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIP 1474
             ::|||||    | |::          | |:        |::|: |  :|:|::|:||::|
Db   569 WMAPEVVKQTMHIEKTDIWSLGCLVIEMLTSKHPY---PNCDQMQAIFRIGE-NILPEFP 624

Qy  1475 SHLSPGLRDVALRCLELQPQDRPPSRELLKHP 1506
             |: |:    |:| |  |:|  || |  |:| ||
Db   625 SNISSSAIDFLEKTFAIDCNLRFTASELLSHP 656

Qy   917 ATKLS--ASSEDI------SERLASIS-VGPSSSTTTTTTTEQPKMVQTKGRPHSQCL 967
             |||||  ||||:        :||:|:||   :::||
Db   127 ATNLEPLPSLEDLDNTVFGAERKKRLSIIGPTSRDRSSPPPGYIPDELHQVARNGSFTSI 186

Qy   968 NSS------PLSHHSQLMFPALSTP----SSSTPSV--PAGTATDVSKHRLQGFIPCRIPSA 1017
             || |         :||:|::|| ||        |     ||  | |:||  || ||:| |
Db   187 NSEGEFIPESMEQMLDPLSLSSPENSGSGSCPSLDSPLGG-------ESYPKSRMPRA 237
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Query Match             6.9%;      Score 536.5;  DB 1;  Length 618;
Best Local Similarity   29.4%;     Pred No. 5.5e-16;
Matches  184;  Conservative  78;  Mismatches 188;  Indels  175;  Gaps  28;
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Qy  1018  S--PQTQRKFSLQFHRNCPENKDSDKLSPVF------TQSRPLPSSNIHRPKPSRPT-P  1067
           :|                                   :|||||||||||||||:|
Db   238  QSYPDNHQEF----------------SDYDNPIFBKFGKGGTYPRRYHVSYHHKDNGRKTFP  284

Qy  1068  GNTSKQGDPSKNSMTLDLNSSKCDDSFGCSNSSNAVIPSDETVFTPVEEKCRLDVNTE  1127
           ||||                         ||| |||  :
Db   285  RARRTQG---NQLTSPV-SFSPTDHSLSTSSGSS--------IFTPEYDSRI---RR  327

Qy  1128  LNSSIEDLLEASMPSSDITVTFKSEVAVLSPEKAENDDTYKDDVNHNQKCKEKMEPAEEEE  1187
           :| |||  :  |:|  |||
Db   328  RGSDID--------NPTLT----VMDISP----------------------------  344

Qy  1188  ALAIAMAMSASQDALPIVPQLQVENGEDIIIIQQDTPETLPGHTKAKQPYREDTEWLKGQ  1247
           :|  :|:           :||                |:|:
Db   345  ----------------------------PSRSP-------RAPTNWRLGK  359

Qy  1248  QIGLGAFSSCYQAQDVGTGTLMAVKQVTYVRNTSSEQEEVVEALREEIRMMSHLNHPNII  1307
           :|:  ||| ||||  :||| : ||||| ||: : |:||||| |||| |||:|:| :|||
Db   360  LLGQGAFGRVYLCYDVDTGRELAVKQVQFDPD-SPETSKEVNALECEIQLLKNFLHERIV  418

Qy  1308  RMLGATC----EKSNYNLFIEWMAGGSVAHLLSKYGAFKESVVINTTEQLLRGLSYLHEN  1363
           |::|       | :|:| :||:||:||:|:||||:        :|||||:|||:|||:|
Db   419  QYYG--CLRDPQEKTLSIFMEYMPGGSIKDQLKAYGALTENGTRKYTRQILEGVHYLHSN  476

Qy  1364  QIHRDVKGANLLIDSTGQRLRIADFGAAARLAS---KGTGAGEFQGQLLGTIAFMAPEV  1420
           |||||:|||||:| :: |||| :|:||| |       || :      :|| ::||||:
Db   477  MILHRDIKGANILRDSTG-NVKLGDFGASKRLQTICLSGTG----MKSVTGTPYWMSPEV  531

Qy  1421  LRGQOYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPG  1480
           |||:|:| : |:||::|| |:||   ||  :|  :|||: |||| |: |  | |||:
Db   532  ISQGYGKKADIWSVACTVVEMLTEKPPW-AEPEA--MAAIFKIATQPTNPKLPPHVSDY  588

Qy  1481  LRDVALRCLELQPQDRPPSRELLKH  1505
           ||  ||| ||| |:|||||:|||:|
Db   589  TRDF-LKRIFVPEAKLRPSADELLRH  612
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RESULT 9
ST11_YEAST
ID   ST11_YEAST    STANDARD;       PRT;     738 AA.
AC   P23561;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine-protein kinase STE11 (EC 2.7.1.-).
GN   STE11 OR YLR362W OR L8039.10.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE OF 22-738 FROM N.A.
RX   MEDLINE=91115076; PubMed=2276621;
RA   Rhodes N., Connell L., Errede B.;
RT   "STE11 is a protein kinase required for cell-type-specific
RT   transcription and signal transduction in yeast.";
RL   Genes Dev. 4:1862-1874(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / AB972;
RA   Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA   Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA   Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA   Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA   Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA   Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
RA   Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
RL   Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   POSSIBLE FUNCTION.
RX   MEDLINE=92331935; PubMed=1628833;
RA   Cairns B.R., Ramer S.W., Kornberg R.D.;
RT   "Order of action of components in the yeast pheromone response
```

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RT   pathway revealed with a dominant allele of the STE11 kinase and the
RT   multiple phosphorylation of the STE7 kinase.";
RL   Genes Dev. 6:1305-1318(1992).
CC   -!- FUNCTION: SERINE/THREONINE PROTEIN KINASE REQUIRED FOR CELL-TYPE-
CC       SPECIFIC TRANSCRIPTION AND SIGNAL TRANSDUCTION IN YEAST. IT
CC       IS THOUGHT THAT IT PHOSPHORYLATES THE STE7 PROTEIN KINASE WHICH
CC       ITSELF, PHOSPHORYLATES THE FUS3 AND OR KSS1 KINASES.
CC   -!- PATHWAY: RESPONSE TO PHEROMONE-INDUCED SIGNAL.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       MAP KINASE KINASE SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC
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CC   or send an email to license@isb-sib.ch).
DR   EMBL; X53431; CAA37522.1; -.
DR   EMBL; U19103; AAB67571.1; -.
DR   PIR; A36456; A36456.
DR   SGD; S0004354; STE11.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR001660; SAM.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00536; SAM; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00454; SAM; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50105; SAM_DOMAIN; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Pheromone response.
FT   DOMAIN       41    105       SAM.
FT   DOMAIN      436    733       PROTEIN KINASE.
FT   NP_BIND     442    450       ATP (BY SIMILARITY).
FT   BINDING     465    465       ATP (BY SIMILARITY).
FT   ACT_SITE    600    600       BY SIMILARITY.
SQ   SEQUENCE   738 AA;   83217 MW;  A50D69800B346A41 CRC64;

Query Match              6.8%;   Score 535;  DB 1;  Length 738;
Best Local Similarity   25.2%;   Pred. No. 7.9e-16;
Matches  205;  Conservative 117;  Mismatches 215;  Indels 276;  Gaps  35;

Qy   781  VSQAEPVEIRYKKLLSLLTFAL----QSIDNSHSMVGKL----SRRIYLSSA-------  824
           |:                       ::: :|  ::: |::
Db   108  IEQVNRLKNLMEKVSSLSTATLSMNSELIPEKHCVIFILNDGSAKKVNVNGCFNADSIKK  167

Qy   825  RMVTTVPHVFSKLLEMLSVSSSTHFTRM-----------RRRLMATADEVEIAEAIQLGV  873
           |::   :|: :|: |: : |:|: |:|             ::: :||: ::|  :
Db   168  RLIRRLPH------ELLATNSNGEVTKMVQDYDVFVLDYTKNVLHLLYDVELVTICH--A  219

Qy   874  EDTLDGGQDSFLQASVPNNYLETTENSSPECTVHLEK---TGKGLCATKLSASSEDISER  930
            :                       :    |              :|
Db   220  NDRVE--------------KNRLIFVSKDQTPS-------DRAISTKKKLYLRTLSALSQ--  258

Qy   931  LASISVGPSSSTTTTTTTTEQPKPMVQTKGRPHS--------QCLNSPLS  973
             ||||                       ||||||
Db   259  ------VGPSSSNL----------LAQNKGISHNNAEGKLRIDNTEKDRIQIFNQRP-  300

Qy   974  HHSQLMFPALSTPSSTPSVPAGTATDVSKHRLQGFIPCRIPSASPQTQRKFSLQFHRNC  1033
           : ||                        :|:  |  |  |:: :: :|::  :|:
Db   301  -----PSEFISTNLAGYFPHTDMKRLQ-----------------------KTMRE------  327

Qy  1034  PENKDSDKLSPVFTQSRPL-PSSNIHRPKFSRPTPGNTSKGGDPSKNSMTLDLNSSSKC  1091
           :  |||  : |:                      :|
Db   328  -SFRHSARLS-IAQRRPLSAESNNI-------------------GD--------  352
```

```
Qy   1092  DDSFGCSSNSSNAVIPSDETVFTPVEEKCRLDVNTELNSSIEDLLEASMPSSDTTVTFKS 1151
                  :  :::                                           |||
Db    353  -----ILLKHSNAV---DMALLQGLDQ------TRLSSKL------DTT----- 381

Qy   1152  EVAVLSPEKAENDDTYKDDVNHNQKCKEKMEAEEEALAIAMAMSASQDALPIVPQLQVE 1211
            : :: ::   :  :           ||   ::  |  |
Db    382  KIPKLAHKRPEDNDAIS-----NQLELLSVESGEEB---------DHDFF--------- 417

Qy   1212  NGEDIIIIQQDTPETLPGHTKAKQPYREDTEWLKGQQIGLGAFSSCYQAQDVGTGTLMAV 1271
            || |:         ||  ||           || :||||||  : :||||:: || :: ||||
Db    418  -GEDSDIV------SLP--TKIATP----KNWLKGACIGSGSFGSVVLGMNAHTGELMAV 464

Qy   1272  KQTYVRNT------------------------------------VVEALRE 1293
           |::| ||                                       :::|:
Db    465  KQVEIKNNNIGVPTDNNKQANSDENNEQEQQBKIEDVGAVSHPKTNQNIHRKMVDALQH 524

Qy   1294  EIRMSHLNHPNIIRMLGATCEKSNYNLFIEWMAGGSVAHLLSKYGAFKESVVINYTEQL 1353
           |:|| |||:||||||||||:|||:|||| |||:||||  | |:|||| ||| ::|||||
Db    525  EMNLLKELHHENIVTYYGASQEGGNLNFLEYVPGGSVSSMLNNYGPFEESLITNFTRQI 584

Qy   1354  LRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIADFGAAARLASKGTGAGEFQGQLLGTI 1413
           |:||  |: |  |||:||||||| || :|:||| || ::|||| : : :  : |||| :
Db    585  LIGVAYLHKKNIIHRDIKGANILIDIKG-CVKITDFGISKKLSPLNKKQNK-RASLQGSV 642

Qy   1414  AFMAPEVLRGQYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAPSI 1473
           |||||||| |  |::||||||| ::|:| || ||   |    ::|:|  :| ::| :
Db    643  FWMSPEVVKQTATTAKADIWSTGCVVIEMFTGKHPF---PDFSQMQAIFKIGTNTT-PEI 698

Qy   1474  PSHLSPGLRDVALRCLELQPQDRPPSRELLKHP 1506
           ||  :: ::  :   |: :   :||| |||| |
Db    699  PSWATSEGKNFLRKAFELDYQYRPSALELLQHP 731
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RESULT 10
M3K2_MOUSE
ID   M3K2_MOUSE     STANDARD;      PRT;   619 AA.
AC   Q61083;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Mitogen-activated protein kinase kinase kinase 2 (EC 2.7.1.-)
DE   (MAPK/ERK kinase kinase 2) (MEK kinase 2) (MEKK 2).
GN   MAP3K2 OR MEKK2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96214986; PubMed=8621389;
RA   Blank J.L., Gerwins P., Elliott E.M., Sather S., Johnson G.L.;
RT   "Molecular cloning of mitogen-activated protein/ERK kinase kinases
RT   (MEKK) 2 and 3. Regulation of sequential phosphorylation pathways
RT   involving mitogen-activated protein kinase and c-Jun kinase.";
RL   J. Biol. Chem. 271:5361-5368(1996).
CC   -!- FUNCTION: PREFERENTIALLY ACTIVATES THE JNK/SAPK GROUP OF MAP
CC       KINASES. PHOSPHORYLATES MEK1 OR JNK MAP KINASE KINASE IN VITRO.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       MAP KINASE KINASE KINASE SUBFAMILY.
CC   --------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; U43186; AAB03536.1; -.
DR   MGD; MGI:1346873; Map3k2.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding.
FT   DOMAIN       356    616       PROTEIN KINASE.
FT   NP_BIND      362    369       ATP (BY SIMILARITY).
FT   BINDING      385    385       ATP (BY SIMILARITY).
FT   ACT_SITE     483    483       BY SIMILARITY.
SQ   SEQUENCE     619 AA;  69835 MW;  799A35218DDE7C41 CRC64;
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Query Match             6.8%;  Score 531;  DB 1;  Length 619;
Best Local Similarity  28.4%;  Pred No. 9.4e-16;
Matches 168;  Conservative  78;  Mismatches 214;  Indels 132;  Gaps  24;

Qy    944  TTTTTEQPKPMVQTKGRPHSQCLNSSPLSHHSQLMFPALSTPSSSTPSVPAGTATDVSK 1003
                :  :::: :   ::           : ::       ::    : ::
Db    124  STQATNLEPSPSPED------------LNNTPLGAERKKRLSVVGPPNRDRSSPPGYIPDILH 175

Qy   1004  H--RLQGFIPCR-----IPSASPQTQRKFSLQFHRNCPENKDSDKLSPVFTQSRPLPSSN 1056
               :  : :      : :::  :  :::  ::  :::   :: :: : :
Db    176  QIARNGSFTSINSEGEFIPESMDQMLDPISL---SSPENSGSGSCPSL---DSPLDGES 228

Qy   1057  IHRPKPSRPTPGNTSKQGDPSKNSMTLDLNSSSKCDDSFGCSS---------NS 1101
              ||     ::                        : : ::        |
Db    229  Y---PKSRMP-----RAQSYPDNHQEFTDYD--NPIFEKFGKGTYPRRYHVSYHHQEYND 279

Qy   1102  SNAVIPSDETVFTPVEEKCRLDVNTELNSSIEDLLEASMPSSDTTVTFKSEVAVLSPEKA 1161
               : ::  :  : ::::       :::    :: ::    ::: :: ::  : ::
Db    280  GRKTFP--------RARRTQGTSFRSPV-----SFSPTDHSLSTSSGSSVFTPE-- 320

Qy   1162  ENDDTYKDDVNHNQKCKEKMEAEEEALAIAMAMSASQDALPIVPQLQVENGEDIIIQQ 1221
                                                               ||
Db    321  ------YDDSRIRRR-------------------------------------GSDI------ 333

Qy   1222  DTPE-TLPGHTKAKQPYREDTEWLKGQQIGLGAFSSCYQAQDVGTGTLMAVKQVTYVRNT 1280
           : :   : :::: :: ::::  ::: :||: :||  :::  : :|||: ::
Db    334  DNPTLTVTDISPPSRSPRAPTNWRLGKLLGQGAFGRVLCYDVDTGRELAVKQVQF-NPE 392

Qy   1281  SSEQEEVVEALREEIRMMSHLNIPNIIRMLGATC----EKSNYNLFIEWMAGGSVAHLLS 1336
           |: ||: ::  ::  :: ::|:|||||  : |||     :|||| |||:||||||  |
Db    393  SPETSKEVNALECEIQLLKNLLHERIVQYG--CLRDPQEKTLSIFMELSPGGSIKDQLK 450

Qy   1337  KYGAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIADFGAAARLA 1396
           :||| ||| |||| :| :|||||||||| |||||||||| |||: |:||| || | : |
Db    451  AYGALTENVTRKYTRQILEGVHYLHSNMIVHRDIKGANILRDSTG-NIKLGDFGASKRLQ 509

Qy   1397  S---KGTGAGEFQGQLLGTIAFMAPEVLRGQYGRSCDVWSVGCAIIEMACAKPPWNAEK 1453
             :    ::   |::|||| ::: |||| :||  | ||| |  ::| |  : |||  ||
Db    510  TICLSGTG---MKSVTGTPYWMSPEVISGEGYGRKADIWSVACTVVEMLTEKPPW-AEF 564

Qy   1454  HSNHLALIFKIASATTAPSIPSHLSPGLRDVALRCLELQPQDRPPSRELLKH 1505
           |||||| |:| ::| | ::||   :::: ::  :||::|| ::||||  || :
Db    565  EA--MAAIFKIATQPTNPKLPPHVSDYTRDF-LKRIFVEAKLRPSAEELLRH 613
```

```
RESULT 11
MKH1_SCHPO
ID   MKH1_SCHPO     STANDARD;      PRT;   1116 AA.
AC   Q10407;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   MAP kinase kinase mkh1 (EC 2.7.1.-).
GN   MKH1 OR SPACIF3.02C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
```

```
Query Match            6.6%;   Score 517.5;  DB 1;  Length 1116;
Best Local Similarity  25.1%;  Pred. No. 6.9e-15;
Matches 185; Conservative 113; Mismatches 287; Indels 153; Gaps 25;

Qy  859 IADEVEIAEAIQLGVEDTLDGQQDSFLQASVPNNYLETIENSSPECTVHLE----------  909
            : :.:  :: :  : :   :    .:  .:  :.:
Db  424 LTSDFEITDA---GPNLSLSGHQ------PDNKYYKGFSSAPNLAVVPELPSRRFRGF  472

Qy  910 ---KTGKGLCATKLSASSEDISERL---------------------ASISVGPSSSTTTTT  946
           :: ::: ::   : :.:                      : :::::::::::::
Db  473 EKIRGAKGEMATKILDATEAQSEKNKFTVCRPHKKVTLKMPLNSGSSAPQSPSSNTSASV  532

Qy  947 TT----TEQPKPMVQTKGRPHSQCLNSSPLSHHSQLMFPALSTPSSSTPSVPAGTATD 1000
          ::        :::::::::::::  : ::::::   ::::::::
Db  533 LTRNFVAHRDPPPPTETSSLRRKNTLTRRPSIRHAR---------SSPYIDTG-HNE  580

Qy 1001 VSKHRLQGFIPCRIPSASPQTQRKFSLQF----HRNCPENKDSDKLSPVFTQSRP---- 1051
           : : : : :: :: :::  :: :  :.         : :::  :: : :: :
Db  581 ASKFSHTSFDP--KASSKSSNSLKESVEALSEIPEDAPALDESDLSGDPFWAIQPKQSS  638

Qy 1052 --LPSSNIHRPKPSRPTPGNTSKQGDPSKNSMTLDLNSSSK---C--DDSFGCSSNSSN 1103
              : :  :::   : :::  :  : : : :::::::      :   ::::::::::
Db  639 SQVPKENHHNIQSKLSI--NTEAATDLKANEL-----SSPKTPEYCRGDDRSISLSPLSY  691

Qy 1104 AVIPSDETVTFPVEEKCRLDVNTELNSSIEDLE---------------ASMPSSD 1144
           : :  :::  : :::  :  :::::::::::
Db  692 RLRKSKHIRESPPSSKVINSGNWEVRPSADDLYEDVDRFFPRYDLDKVLVVDQSRMVSSP  751

Qy 1145 TTVTFK---SEVAVLSPEKAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSASQDA 1201
           : : :       :::::: :   :  : ::  : :::: :
Db  752 SKVSIRPXMKSVRLLAREASE---ARKEIRHNARRNKSGNLLRRSSTKLW----------  798

Qy 1202 LPIVPQLQVENGEDIIIIQQDTPETLPGHTKAKQPYREDTEWLKGQOIGLGAFSSCYQAQ 1261
           :  : :       :: :  : :::::     ::      :::::::::::::
Db  799 ----------GSRIVELKPDTTITSGSVVSQNATFK----WMKGELIGNGTYGKVFLAM  843

Qy 1262 DVGTGTLMAVKQVTYVRNTSSE---QEEVVEALREEIRMMSHLNHPNIIRMLGATCEKS 1317
           ::::::::::::    :::::     ::::::::: ::::::::::::::::::::::::
Db  844 NINTGELIAVKQVEIPQTINGRHDQLRKDIVDSINAEISMIADLDHLNIVQLGFEKTET  903

Qy 1318 NYNLFIEWMAGGSVAHLLSKYGAFKESVVINTEQLLRGLSYLHENQIIHRDVKGANLLI 1377
           ::  : : ::: ::      :: : ::  : : ::::::::::::::::::::::::::
Db  904 DISIFLEYVSGGSIGRCLRNYGPFEEQVRFVSRQVLYGLSYLHSKGIIHRDLKADNLLI  963

Qy 1378 DSTGQRLRIADFGAAARLASKGTGAGEFQGQLLGTIAFMAPEVLRG--QQYGRSCDVWSV 1435
           :::::::::::::::::    : :::: :: ::::::::::::::     ::::::::::
Db  964 DFDGV-CKISDFGISKH--SDNVYDNDANLSMQGSIFWMAPEVIHNDHQGYSAKVDVWSL 1020

Qy 1436 GCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHL---SPGLRDVALRCLEL 1491
           :: ::::::  ::::    ::  : :::::::: ::::: : :       : ::: :::
Db 1021 GCVVLEMLAGRRPWSTDE--AIQAMFKLGTEKKAPPISELVSQVSPEAIQFLNACFTV 1077

Qy 1492 QPQDRPPSRELLKHPVFR 1509
           :::::::::::::::  :
Db 1078 NADVRPTAEELLNHPFMK 1095
```

RESULT 12
M3K4_HUMAN
ID   M3K4_HUMAN   STANDARD;   PRT; 1607 AA.
AC   Q9Y6R4; Q92612;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Mitogen-activated protein kinase kinase kinase 4 (EC 2.7.1.-)
DE   (MAPK/ERK kinase kinase 4) (MEK kinase 4) (MEKK 4) (MAP three kinase
DE   1).
GN   MAP3K4 OR MAPK4 OR MEKK4 OR MTK1 OR KIAA0213.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]

RP   SEQUENCE FROM N.A.
RC   STRAIN=SP66;
RX   MEDLINE=97342589; PubMed=9199286;
RA   Sengar A.S., Markley N.A., Marini N.J., Young D.;
RT   "Mkh1, a MEK kinase required for cell wall integrity and proper
RT   response to osmotic and temperature stress in Schizosaccharomyces
RT   pombe.";
RL   Mol. Cell. Biol. 17:3508-3519(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purneile B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).

-!- FUNCTION: MAY REGULATE CELL MORPHOLOGY, CELL WALL INTEGRITY, SALT
CC   RESISTANCE, CELL CYCLE REENTRY FROM STATIONARY-PHASE ARREST, AND
CC   FILAMENTOUS GROWTH IN RESPONSE TO STRESS. ACTIVATES THE MAP KINASE
CC   KINASE SKH1/PEK1 BY PHOSPHORYLATION.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   MAP KINASE KINASE KINASE SUBFAMILY.

DR   EMBL; U53872; AAB62319.1; -.
DR   EMBL; Z70690; CAA94620.1; -.
DR   HSSP; Q00534; 1BI8.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR001660; SAM.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00454; SAM; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding.
FT   DOMAIN   825   1094   PROTEIN KINASE.
FT   NP_BIND   831   839   ATP (BY SIMILARITY).
FT   BINDING   854   854   ATP (BY SIMILARITY).
FT   ACT_SITE   955   955   BY SIMILARITY.
SQ   SEQUENCE   1116 AA; 125132 MW; 7AFDB3EC62EED47B CRC64;

```
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS OF LYS-1371.
RC   TISSUE=Fetal liver, and Skeletal muscle;
RX   MEDLINE=97449143; PubMed=9305639;
RA   Takekawa M., Posas F., Saito H.;
RT   "A human homolog of the yeast Ssk2/Ssk22 MAP kinase kinase kinases,
RT   MTK1, mediates stress-induced activation of the p38 and JNK
RT   pathways";
RL   EMBO J. 16:4973-4982(1997).
RN   [2]
RP   SEQUENCE OF 68-1607 FROM N.A. (ISOFORM B).
RC   TISSUE=Bone marrow;
RX   MEDLINE=97191544; PubMed=9039502;
RA   Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
RA   Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT   "Prediction of the coding sequences of unidentified human genes. VI.
RT   The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT   analysis of cDNA clones from cell line KG-1 and brain.";
RL   DNA Res. 3:321-329(1996).
CC   -!- FUNCTION: ACTIVATES THE CSBP2, P38 AND JNK MAPK PATHWAYS, BUT NOT
CC       THE ERK PATHWAY. SPECIFICALLY PHOSPHORYLATES AND ACTIVATES MAP2K4
CC       AND MAP2K6.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN HEART, PLACENTA,
CC       SKELETAL MUSCLE AND PANCREAS, AND AT LOWER LEVELS IN OTHER
CC       TISSUES.
CC   -!- DOMAIN: THE N-TERMINAL NON-CATALYTIC DOMAIN (1-606) CONTAINS AN
CC       ESSENTIAL DOMAIN FOR THE DOMINANT-INHIBITORY EFFECT.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       MAP KINASE KINASE KINASE SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF002715; AAB60804.1; -.
DR   EMBL; D86968; BAA13204.1; -.
DR   HSSP; P24941; 1HCL.
DR   Genew; HGNC:6856; MAP3K4.
DR   MIM; 602425; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Alternative splicing.
FT   DOMAIN        4       7       POLY-ALA.
FT   DOMAIN       25      38       POLY-PRO.
FT   DOMAIN     1190    1201       POLY-ALA.
FT   DOMAIN     1342    1600       PROTEIN KINASE.
FT   NP_BIND    1348    1355       ATP (BY SIMILARITY).
FT   BINDING    1371    1371       ATP (BY SIMILARITY).
FT   ACT_SITE   1462    1462       BY SIMILARITY.
FT   VARSPLIC   1175    1223       MISSING (IN ISOFORM B).
FT   MUTAGEN    1371    1371       K->R: LOSS OF ACTIVITY.
FT   CONFLICT    791     791       I -> R (IN REF. 2).
SQ   SEQUENCE   1607 AA;  181550 MW;  24BC459773005287 CRC64;
```

Query Match   6.4%;   Score 502.5; DB 1;   Length 1607;
Best Local Similarity 19.7%;   Pred. No. 4.5e-14;
     Matches 288; Conservative 239; Mismatches 574; Indels 363; Gaps 59;

```
Qy   169 TLKGLHKMDDRPEERMIREKLKATCMPAWKHEWL---ERRNRR------------------- 208
         ||||:|:|| :|||  :     ||    |:  ||        |:
Db   370 SLQALQKDYEKYAAKFDQDRVQALCL------WLNITKDLNQKLRIMGTVLGIKNLSDIG 423
```

Qy   209 GPVVVKPIPVKGDGSEMNHLAAESPGEVQASAASPASKGRRSPSPGNSPSGRTVKSESPG 268
         || || ||| : | : |||: |: :::|:: |||::| || ||: |::||
Db   424 WPVFEIPSPRPSKGNEPEYEGDDTEGELKELESS----------------TDESEEEQ 465

Qy   269 VRRKRVSPVPFQSGRITPPRRAPSPDGFSPYSPEETNRRVNKVMRARLYLLQQIGPNSFL 328
         : | || :| ::| | | | : | :   : : :::: |:::
Db   466 ISDPRV-------PEIRQPIDNSFDIQSRDCISKK----------------LERLESEDDS 503

Qy   329 IGGDSPDNKYRVFIGPQNCSCARGTFCIHLLFVMLRVFQLEPSDPMLWRKTLKNFEVESL 388
         : | |: | |:| | : | : : :: : :| : | :|| | |:
Db   504 LGWGAPD--------WSTEAG-FSRHCLTSIYRPFV-------DKALKQMGLRKL 542

Qy   389 FQKYHS-------RRSSRIKAPSRNTIQKFVSRMSNSHTLSSSTSTSSSE--NSIKDE 438
         |:|: | | | | |:| : | ::: | :::: :| :::
Db   543 ILRLHKLMDGSLQRARIALVKNDRPVEFSEFPDPMWGSDYVQLSRTPPSSEEKCSAVSWE 602

Qy   439 EEQMCPICLLGMLD----EESLTVCEDGCRNKLH--HICMSIWAEECRRNREPLICPL-- 490
         | | |:   : || | | : :| ||| | | |
Db   503 E-------LKAMDLPSFEPAFLVL--CRVLLNVIHECLKLRLEQ-RPAGEPSLLSIKQ 650

Qy   491 ---CRSKWRS-----HDFYSHELSSPSVDSPSSLRAAQQQTVQQQPLAGSRRNQESNF 539
            :| || |: : | :| | |||: | :::: ::: :: | |:: |:
Db   651 LVRECKEVLKGGLLMKQYYQFMLQEVLEDLEKP-----------------DCNI 687

Qy   540 NLTHYGTQQIPPAYKDLAEPWIQVF------GMELVGCLFSRWWN----------VR--EMAL 584
         :| | ||| | | | :|: |:| | | || :|||
Db   688 DAFEEDLHKMLMVYFDYMRSWIQMLQQLPQASHSLKNLLEEEWNFTKEITHYIRGGEAQA 747

Qy   585 RRLSHDVSGALLLANGESTGNSGGSSGSSPSGGATSGSGSQTSISGDVVEACCSVLSMVCA 644
         : | |: | ::|::||| :| : | | | :: : :|| | | | | :|: :
Db   748 GKLFCDIAGMLLKSTGSFLEFGLQESCAEFWTSADDSASDEIIRSVIE-----ISRALK 802

Qy   645 DPVYKVYVAALKTLRAMLVYTPCHSLAERILQRLLQPVVDTI-----LVKCADANSRTSQ 700
         :   : :| | : || :| | | |: | :::   : ||
Db   803 ELFHEARERASKALGFAKMLRKDLEIAAEFRLSAPVRDLLDVLVLKSKQYVKVQIPGLENLQ 862

Qy   701 LSISTLLELCKGQAGELAVGREILKAGSIGIGGVD-----------YVLNCILGNQTES 748
         : : | : | | :| || | | : | :|: |:
Db   863 MFVPDTL-------AEEKSIILQLLNAAA----GKDCSKDSDDVLIDAYLLLTKHGDRARD 912

Qy   749 N-----NWQELLGRLCLIDRLLLEFPAEFYPHIVSTDVSQAEPVEIRYKKLLSLLTFALQ 803
         :   : | | | :|: | | |:   : :| :| : :| :::: :|
Db   913 SEDSWGTWEAQ-----------PVKVVPQVETVDTLRSMQVD-------NLLLVMQ 951

Qy   804 SIDNSHSMVGKLSRRIYLSSARMVTTV---------PHVFSKLLEMLSVSSSTHFTRMRRRL 856
         :::: : ||:: | ::| : | || | : | :::|
Db   952 S---AHLTI---QRKAFQQSIEGLMTLCQEQTSSQPVIAKALQQLK----------991

Qy   857 MAIADEVEIAEAIQLGVEDTLDGQQDSFLQASVPNNYLETTENSSPECTVHLEKTG----912
         : :| :| | | : :: | | :| : | ||| |:| :
Db   992 ---NDALELCNRISNAI-DRVDHMFTSEFDAEVDESESVTLQQYYREAMIQGYNFGFEYH 1047

Qy   913 KGLCATKLSASSEDISERLASISVGPSSSTTTTTTEQPKPMVQTKGRPHSQCLNSSPL 972
         | | |:| |: : | | ::::|: | || :|
Db 1048 KEVVRLMSGEPRQKIGDKYISFARKWMNYVLTKCESGRGTRPRWATQGFDFLQAIEPAFI 1107

Qy   973 SHHSQLMFPALSTPSSSTPSVPAGTATDVSKHRLQGFIPCRIPSASPQTORKFSLQFHRN 1032
         : : :| :| :| |: | :| | | : : || : : ||:   :|:|:
Db 1108 SALPEDDFLSLQALMNECIGHVIG-----KPH--------SPVT--GLYLAIHRN 1147

Qy 1033 CPENKDSDKLSPVFTQSRPL---------PSSNIHRKP---SRPTPGNTSKQGDPSKN 1079
         | : |:|| ||| | | |: |:|| |:| | | : ||
Db 1148 SP------------RPMKVPRCHSDPPNPHLIIPTPEGFSTRSMPSDARSHGSPAAA 1192

Qy 1080 SMTLDLNSSSKCDDSFGCSSNSSNAVIPSDETVFTPVEEKCRLDVNTELNSSIEDLLEAS 1139
         : : | |:: |:| : || :: | | :| :: : :|::
Db 1193 AAAAAVAASRPSPSGG-------DSVLPKS-----------ISSAHDTRGSS 1227

Qy 1140 MPSSDTTVTFKSEVAV------LSPEKAENDDTYK--DDVNHNQCKE--KMEAEEEAL 1189
         :|:|| || | | | |: |:: | :: || | :| |
Db 1228 VPENDRLASIAAELQFRSLSRHSSPTEERDEPAYPRGDSSGSTRRSWELRTLISQSKDTA 1287
```

```
Qy   1190 AIAMAMSASQDALPIVPQLQVENGEDIIIIQQ--DTPETLPG--HTKAKQPYREDTEWLK 1245
          : :  :   | |:      :  ::     : |:         | :| :| :| :
Db   1288 SKLGPIEAIQKSVRLFEEKRYREMRRKNIIGQVCDTPKSYDNVMHVGLR---KVTFKWQR 1344

Qy   1246 GQQIGLGAFSSCYQAQDVGTGTLMAVKQVTYVRNTSSEQDEVVEALREEIRMSHLNHPN 1305
          |  | | |   ||   :  | ||| |:| :           :    :|: |||:|:||
Db   1345 GNKIGEGQYGKVYTCISVDTGELMAMKEIRFQPN----DHKTIKETADELKIFEGIKHPN 1400

Qy   1306 IIRMLGATCEKSNYNLFIEWMAGGSVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQI 1365
          ::| :|   | : |:|:|  : |:  :||:|:  :    |: :  ::  :| |:::|| |
Db   1401 LVRYFGVELHREEMYIFMEYCDEGTLEE-VSRLG-LQEHVIRLYSKQITIAINVLHEHGI 1458

Qy   1366 IHRDVKGANLLIDSTGQRLRIADFGAAARLASKG-TGAGEFQGQLLGTIAFMAPEVL--- 1421
          :|||:||||:::::: |:|::|||| :|| :  | : :||  :  |  | :|||||:
Db   1459 VHRDIKGANIFLTSSG-LIKLGDFGCSVKLKNNAQTMPGEV-NSTLGTAAYMAPEVITRA 1516

Qy   1422 RGQQYGRSCDVWSVGCAIIEMACAKPWNAEKHSNHLALIPKIASATTAPSIPSHLSPGL 1481
           |  :||: ||| |||:|||: | :||: |:   :    |:  |:    |:| || ::|
Db   1517 KGEGHGRAADIWSLGCVIEMVTGKRPWHEYEH--NFQIMYKVGMG-HKPPIPERLSPEG 1573

Qy   1482 RDVALRCLELQPQDRPPSRELLKH 1505
           || : ||| ::  ||::   |:|
Db   1574 KDFLSHCLESDPKMRWTASQLLDH 1597
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RESULT 13
M3K4_MOUSE
ID   M3K4_MOUSE   STANDARD;   PRT;   1597 AA.
AC   O08648; O08649; O70124;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Mitogen-activated protein kinase kinase kinase 4 (EC 2.7.1.-)
DE   (MAPK/ERK kinase kinase 4) (MEK kinase 4) (MEKK 4).
GN   MAP3K4 OR MEKK4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC   TISSUE=Brain;
RX   MEDLINE=97236778; PubMed=9079650;
RA   Gerwins P., Blank J.L., Johnson G.L.;
RT   "Cloning of a novel mitogen-activated protein kinase kinase kinase,
RT   MEKK4, that selectively regulates the c-Jun amino terminal kinase
RT   pathway.";
RL   J. Biol. Chem. 272:8288-8295(1997).
RN   [2]
RP   SEQUENCE OF 363-1049 FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Ectoplacental cone;
RX   MEDLINE=97422605; PubMed=9288631;
RA   Schweifer N., Valk P.J., Deiwel R., Cox R., Francis F.,
RA   Meier-Ewert S., Lehrach H., Barlow D.P.;
RT   "Characterization of the C3 YAC contig from proximal mouse chromosome
RT   17 and analysis of allelic expression of genes flanking the imprinted
RT   Igf2r gene.";
RL   Genomics 43:285-297(1997).
CC   -!- FUNCTION: ACTIVATES THE CSBP2, P38 AND JNK MAPK PATHWAYS, BUT NOT
CC   THE ERK PATHWAY. SPECIFICALLY PHOSPHORYLATES AND ACTIVATES MAP2K4
CC   AND MAP2K6.
CC   -!- SUBCELLULAR LOCATION: LOCALIZED IN PERINUCLEAR VESICULAR-LIKE
CC   STRUCTURES, PROBABLY GOLGI-ASSOCIATED VESICLES.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
CC   PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGH EXPRESSION WAS FOUND IN
CC   SKELETAL MUSCLE, KIDNEY, TESTIS FOLLOWED BY HEART BRAIN AND LUNG.
CC   LOW EXPRESSION WAS FOUND IN SPLEEN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   MAP KINASE KINASE SUBFAMILY.

DR   EMBL; U85607; AAC53126.1; -.
DR   EMBL; U85608; AAC53127.1; -.
DR   EMBL; U66240; AAC08286.1; -.
DR   HSSP; P24941; 1HCL.
DR   MGD; MGI:1346875; Map3k4.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Alternative splicing;
FT   DOMAIN   1178   1182   POLY-ALA.
FT   DOMAIN   1332   1590   PROTEIN KINASE.
FT   NP_BIND   1338   1345   ATP (BY SIMILARITY).
FT   BINDING   1361   1361   ATP (BY SIMILARITY).
FT   ACT_SITE 1452   1452   BY SIMILARITY.
FT   VARSPLIC 1162   1213   MISSING (IN ISOFORM B).
FT   CONFLICT   363   364   SL -> NS (IN REF. 2).
FT   CONFLICT   473   473   T -> A (IN REF. 2).
SQ   SEQUENCE   1597 AA; 179948 MW; E84AEAAE92D103A4 CRC64;

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Query Match             6.1%;
Best Local Similarity   20.4%;     Score 475; DB 1; Length 1597;   Pred. No. 6.4e-13;
Matches   301;  Conservative   211;  Mismatches   576;  Indels   386;  Gaps   66;

Qy   169 TLKGLHKMDDRPEERMIREKLKATCMPAWKHEWL--ERRNRRGPVVVKPIPVKGDGSEM 225
         :|:||  :|:  ::|:|:  |:|::||:: :| :| :| ::  || |::|:: :
Db   363 SLQALQKDYERYAAKDFEDRVQALCL------WLNITKDLNQKLRIMGTVLGIK-NLSDI 415

Qy   226 NHLAAESPGEVQASAASPASKGRRSPSPGNSPSGRTVKSE-----SPGVRRKRVSPVPF 279
         | |  |     :|  ||::|     |  ||:  ||:: :|             :::|:
Db   416 GWPVFEIP--------SP-----RPSKGYEPEDEVEDTEVELRELESGTEESDEEPTP- 460

Qy   280 QSGRITPPRRAFSPDGFSPYSPE------ET--NRRVNKVMRARLYLLQQIGPNSFLIGG 331
         :  :| | | |  |  ||:||            ||  ||  |  :  |    ::
Db   461 ------------SPRVPELRLSTDTILDSRSQGCVSRK---LERLESEEDSIGW 499

Qy   332 DSPDNKYRVFIGPQNCSCARGTFCIHLLFVMLRVFQLEPSDPMLWRKTLKNFEVESLFQK 391
         || : |  | |  |  :| :|    |    | |  |  |       |    :|: |||
Db   500 GTAD-------CGPE--ASR----HCLTSIYRPFV--------DKALKQMGLRKLLIR 536

Qy   392 YHS------RRSSRIKAPSRNTIQKFVSRMSNSHTLSSSSTSTSSSENSIKDEEQMC 443
         |:|      |:| :|| | | :|  :| ::| |::|:  ::::||::::::
Db   537 LHKLMNGSLQRARVALVKDDRPVEFSDFPGPMWGSDYVQLSGTPPSS---------EQKC 587

Qy   444 PICLLGMLDEESLIVCEDG----CRNKLH--HHCMSIWAEECRRNREPLICPL------C 491
         || :| : : |      |     |:  | :   ||:|     | |  :  :|
Db   588 SAVSWEELRAMDLPSFEPAFLVLCRVLLNVIHECLKLRLEQ-RPAGEPSLLSIKQLVREC 646

Qy   492 RSKWRSHDFYSHELLSSPVDSPSSLRAAQQTVQQQPLAGSRRNQESNFNLTHYGTQQIPP 551
         || |:  :|:  |:|:||  ||:: |    :  |         :::     |::| :|:
Db   647 KEVLK----------------------GGLLMKQYQFMLQEVLGGLEKTDCNMDAFEEDLQKMLM 690

Qy   552 AYKDLAEPWIQVF------GMELVGCLFSRNWN--------VR-EMALRLSHDVSGALL 596
         | | | |  | |       ||:|  |:| |         |: :||:|||:|:: |::
Db   691 VYFDYMRSWIQMLQQLPQASHSLKNLLEEWNTKEITHYIRGEAQAGKLFCDIAGMLL 750

Qy   597 LANGE--------------------STGNSGGSS----- 618
         |  |                     |:|| ||
Db   751 KSTGSFLESGLQESCAELWTSADDNGAADELRRSVIEISRALKELFHEARERASKALGFA 810

Qy   619 TSGSSQTSISGDVVEACCS--VLSMVCADPVYKVYVAALKTLRAMLVYTPCHSLAERIKL 676
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Db   811  KMLRKDLEIAAEFVLSASARELLDALKAKQVVKVQIPGLENLH---VFVP-DSLAEEKKI  866

Qy   677  QRLLQPVVDTIIVKCA---DANSRTQLSISTLLELCKGQAGELAVGREILKAGSIGIGG  733

Db   867  --ILQ-----LLNAATGKDCSKDPDDVFMDAFLLLTK--HGDRA-------------  901

Qy   734  VDYVLNCILGNQTESNNWQELLGRLCLIDRLLLEFPAEFYPHIVSTDVSQAEPVE-IRYK  792

Db   902  ---------RDSEDGWGTWEARAVKI------------VPQVETVDTLRSM  931

Qy   793  KLLSLLTFALQSIDNSHSMVGKLSRRIYLSSARMVTTVPH------VFSKILEMLSVSS  845

Db   932  QVDNLLLVVMES---AHLV---LQRKAFQQSIEGLMTVRHEQTSSQPIIAKGLQQLK---  982

Qy   846  STHFTRMRRRLMAIADEVEIAEAIQLGVEDTLDGQQDSF--LQASVPNNYLETTENSSP  902

Db   983  --------------NDAIELCNRI----SDAIDRVDHMFTLEFDAEVEESESATLQQYYR  1024

Qy   903  ECTVHLEKTG---KGLCATKLSASSEDISERLASISVGPSSSTTTTTTTEQPKPMVQT  958

Db   1025 EAMIQGYNFGFEYHKEVVRLMSGEFRQKIGDKYISFAQKWMNVVLTKCESGRGTRPRWAT  1084

Qy   959  KGRPHSQCLNSSPLSHHSQLMFPALSTPSSSTPSVPAGTATDVSKHRLQGFIPCRIPSAS  1018

Db   1085 QGPDFLQAIEPAFISALPEDDFLSLQALMNECIGHVIG-----KPH------------S  1126

Qy   1019 PQTQRKFSLQFHRRNCPENKDSDKLSPVFTQSRPLPSSNIHRPKPSR----PTPGNTSKQG  1074

Db   1127 PVT------AIHRNSP-------RPVKVPRCHSDDPNPHLIIPTPEGFSTRS  1165

Qy   1075 DPSK------NSMIDLNSSSKCDDSFGCSSNSSNAVIPSDETVFTPVVEBKCRLDVNIELN  1129

Db   1166 VPSDARTHGNSVAAAAAVRAAATTAAGRPGPGGGDSVPAK----------PVNI---  1209

Qy   1130 SSIEDLLEASMPSSDTTVTFKSEVAV-----LSPEKAENDDTY--KDDVNHHNQKCKE--  1179

Db   1210 --APDTRGSSVPENDRLASIAAELQFRSLSRHSSPTEERDEPAYPRSDSSGSTRRSWELR  1267

Qy   1180 KMEAEEERALAIAMAMSASQDALPIVPQLQVENGEDIIIIQQ--DTPETLPG--HTKAKQ  1235

Db   1268 TLISQTKDSASKQGPIEAIQKSVRLFEERRYREMRRKNIIGQVCDTPKSYDNVMHVGLR-  1326

Qy   1236 PYREDTEWLKGQQIGLGAFSSCYQAQDVGTGTLMAVKQVTYVRNTSSEQEEVVEALREEI  1295

Db   1327 --KVTFKWQRGNKIGEGQYGKVYTICISVDTGELMAMKEIRFQPN----DKHTIKETADEL  1380

Qy   1296 RMMSHLNHPNIIRMLGATCEKSNYNLFIEWMAGGSVAHLLSKYGAFKESVVINYTEQLLR  1355

Db   1381 KIFEGIKHPNLVRYFGVELHREEMYIFMEYCDEGTLEE-VSRLG-LQEHVIRLYTKQITV  1438

Qy   1356 GLSYLHENQIIHRDVKGANLLIDSTGQRLRIADFGAAARLASKG-TGAGEFQGGLLGTIA  1414

Db   1439 AINVLHEHGIVHRDIKGANIFLTSSG-LIKLGDFGCSVKLKNNAQTMPGEV-NSTLGTAA  1496

Qy   1415 FMAPEVL---RGQQYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAP  1471

Db   1497 YMAPEVITRAKGEGHGRAADIWSLGCVVIEMVTGKRPWHEYEH--NFQIMYKVGMG-HKP  1553

Qy   1472 SIPSHLSPGLRDVALRCLELQPQDRPPSRELLKH  1505

Db   1554 PIPERLSPEGKAFLSHCLESDPKIRWTASQILDH  1587
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RESULT 14
WIS4_SCHPO
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ID   WIS4_SCHPO     STANDARD;      PRT;   1401 AA.
AC   O14299; P87062; Q92384;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   MAP kinase kinase kinase wis4 (EC 2.7.1.-) (MAP kinase kinase kinase
DE   wak1) (MAP kinase kinase wik1).
GN   WIS4 OR WAK1 OR WIK1 OR SPAC9G1.02.
```

```
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98026892; PubMed=9321395;
RA   Samejima I., Mackie S., Fantes P.A.;
RT   "Multiple modes of activation of the stress-responsive MAP kinase
RT   pathway in fission yeast.";
RL   EMBO J. 16:6162-6170(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
RN   [3]
RP   SEQUENCE OF 96-1401 FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=97282620; PubMed=9136929;
RA   Shieh J.C., Wilkinson M., Buck V., Morgan B., Makino K.,
RA   Millar J.B.A.;
RT   "The Mcs4 response regulator coordinately controls the stress-
RT   activated Wak1-Wis1-Sty1 MAP kinase pathway and fission yeast cell
RT   cycle.";
RL   Genes Dev. 11:1008-1022(1997).
RN   [4]
RP   SEQUENCE OF 457-543 FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=97331762; PubMed=9188094;
RA   Shiozaki K., Shiozaki M., Russell P.;
RT   "Mcs4 mitotic catastrophe suppressor regulates the fission yeast cell
RT   cycle through the Wik1-Wis1-Spc1 kinase cascade.";
RL   Mol. Biol. Cell 8:409-419(1997).
CC   -!- FUNCTION: INVOLVED IN A SIGNAL TRANSDUCTION PATHWAY THAT IS
CC       ACTIVATED IN UNDER CONDITIONS OF HEAT SHOCK, OXIDATIVE STRESS OR
CC       LIMITED NUTRITION. UNLIKE WIN1, IT IS NOT ACTIVATED BY CHANGES IN
CC       THE OSMOLARITY OF THE EXTRACELLULAR ENVIRONMENT. ACTIVATES THE
CC       WIS1 MAP KINASE KINASE BY PHOSPHORYLATION.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       MAP KINASE KINASE KINASE SUBFAMILY.
```

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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; Z98763; CAB11500.1; -.
DR   EMBL; Y07750; CAA69030.1; ALT_INIT.
DR   EMBL; Y11989; CAA72718.1; -.
DR   EMBL; U81521; AAB39752.1; -.
DR   HSSP; P24941; 1CKP.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding.
FT   DOMAIN       1306      PROTEIN KINASE.
FT   NP_BIND      1037   1051   ATP (BY SIMILARITY).
FT   NP_BIND      1043   1051   ATP (BY SIMILARITY).
FT   BINDING      1066   1066   ATP (BY SIMILARITY).
FT   ACT_SITE     1161   1161   BY SIMILARITY.
FT   CONFLICT      484    485   RL -> SP (IN REF. 3).
FT   CONFLICT     1346   1346   D -> V (IN REF. 1).
SQ   SEQUENCE   1401 AA;  160537 MW;  529A989D2B627F3D CRC64;

Query Match             5.5%;  Score 433.5; DB 1;  Length 1401;
Best Local Similarity  27.8%;  Pred. No. 3e-11;  Gaps 61;
  Matches 119;  Conservative  86;  Mismatches 162;  Indels 16;

Qy  1103 NAVIPSDETVFTVPEEKCRLDVNTELNSSIEDLLEASMPSSDTTVTFKSEVAVLSPEKAE 1162
              :  ||:| ||  ::  ||   :  ||   :|:||    :|  :|||
Db   914 NNILLIDDAMFLKIREK------VGKSMAFLL-----THFDVLGAKSKVAA----KLQ  956

Qy  1163 NDDTYKDDVNHNQKCKEKMEAEEEALAIAMAMSASCDALPIVPQLQVENGEDIIIIQQD 1222
                  :  :| ::|| ||:|                 |: :||:   :|: |:||
Db   957 REST--EVSSSPRLTSFGDV-EEEALSIQL--LQKETMLRIDELEIERNNTLL---- 1004

Qy  1223 TPETLP-GHTKAKQPYRE---------DTEWLKGQOIGLGAFSSCYQAQDVGTGTL 1268
              :                           :  |||||||  :|  |  : |
Db  1005 --ERLAIGHVLDDSVFRNRDFIKLASSFSNITIRWQQGHFVRSGMFGDVYTGVNMETGDL 1062

Qy  1269 MAVKQVTYVRNTSSEQEEVRALREEIRMMSHLNHPNIIRMLGATCEKSNYNLFIEWMAG 1328
            ||||:||      :  || |   :  | ||||||:| |   :    | ||||:|:|
Db  1063 LAVKEIKL--QDSRTFRSTVDQIHNEMTVLERLNHPNVVTYYGVEVHREKVVIFMEFCQG 1120

Qy  1329 GSVAHLLSKYGAFKESVVINYTEQLLRGLSLYLHENQIIHRDVKGANLLIDSTGQRLRIAD 1388
           |: | ||:  |  :  ::| ||| ||:|:|| |||:|||||:| || ||:|  |:| :|
Db  1121 GSLADLLAHGRIEBDENVLKVYVVQLLEGLAYIHSQHLHRDIKPANILLDHRGM-IKYSD 1179

Qy  1389 FGAAARLASKGTGAGEFQG------QLLGTIAFMAPEVLRGGQYG--RSCDVWSVGCAII 1440
           ||:   :        ::|       ||||  :|||||:| |   |    ||||| ||:|
Db  1180 FGSALYVSPPTDPEVRYEDIQPELQHLAGTPMYMAPEIILGTKKGDFGAMDIWSLGCVIL 1239

Qy  1441 EMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSH--LSPGLRDVALRCLELQPQDRPP 1498
           || | |:||||| ||:||||||:||| |||| ||::   |||| || | | |||:|||:
Db  1240 EMMTGSTPWS--EMDNEWAIMTHVAAMHT-PSIPQNEKISSLARDFIEQCFERDPEQRPR 1296

Qy  1499 SRELLKHP 1506
           : || ||
Db  1297 AVDLLTHP 1304

RESULT 15
M3K5_HUMAN
ID   M3K5_HUMAN     STANDARD;      PRT;   1374 AA.
AC   Q99683; Q99461;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Mitogen-activated protein kinase kinase kinase 5 (EC 2.7.1.-)
DE   (MAPK/ERK kinase kinase 5) (MEK kinase 5) (MEKK 5) (Apoptosis signal-
DE   regulating kinase 1) (ASK-1).
GN   MAP3K5 OR MAPKKK5 OR MEKK5 OR ASK1.
```

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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97094945; PubMed=8940179;
RA   Wang X.S., Diener K., Jannuzzi D., Trollinger D., Tan T.-H.,
RA   Lichtenstein H., Zukowski M., Yao Z.;
RT   "Molecular cloning and characterization of a novel protein kinase with
RT   a catalytic domain homologous to mitogen-activated protein
RT   kinase kinase.";
RL   J. Biol. Chem. 271:31607-31611(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97130104; PubMed=8974401;
RA   Ichijo H., Nishida E., Irie K., ten Dijke P., Saitoh M., Moriguchi T.,
RA   Takagi M., Matsumoto K., Miyazono K., Gotoh Y.;
RT   "Induction of apoptosis by ASK1, a mammalian MAPKK that activates
RT   SAPK/JNK and p38 signaling pathways.";
RL   Science 275:90-94(1997).
RN   [3]
RP   SEQUENCE OF 419-1374 FROM N.A.
RA   Phillips S.;
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PHOSPHORYLATES AND ACTIVATES TWO DIFFERENT SUBGROUPS OF
CC       MAP KINASE KINASES, MKK4/SEK1 AND MKK3/MAPKK6 (OR MKK6), WHICH IN
CC       TURN ACTIVATED STRESS-ACTIVATED PROTEIN KINASE (SAPK, ALSO KNOWN
CC       AS JNK; C-JUN AMINO-TERMINAL KINASE) AND P38 SUBGROUPS OF MAP
CC       KINASES, RESPECTIVELY. OVEREXPRESSION INDUCES APOPTOTIC CELL
CC       DEATH.
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART AND PANCREAS.
CC   -!- INDUCTION: BY TNF-ALPHA.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       MAP KINASE KINASE KINASE SUBFAMILY.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; U67156; AAC50894.1; -.
DR   EMBL; D84476; BAA12684.1; -.
DR   EMBL; AL024508; CAA19711.1; -.
DR   HSSP; Q63450; 1A06.
DR   Genew; HGNC:6857; MAP3K5.
DR   MIM; 602448; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding; Apoptosis.
FT   DOMAIN        680    938   PROTEIN KINASE.
FT   NP_BIND       686    693   ATP (BY SIMILARITY).
FT   BINDING       709    709   ATP (BY SIMILARITY).
FT   ACT_SITE      803    803   BY SIMILARITY.
FT   CONFLICT      763    763   S -> Y (IN REF. 2).
FT   CONFLICT      959    959   N -> NA (IN REF. 2).
FT   CONFLICT     1308   1308   T -> I (IN REF. 2).
SQ   SEQUENCE   1374 AA;  154536 MW;  265BDC65968AF985 CRC64;

Query Match             5.5%;  Score 430.5; DB 1;  Length 1374;
Best Local Similarity  36.6%;  Pred. No. 4e-11;
  Matches  96;  Conservative  97;  Mismatches  48;  Indels 21;  Gaps  7;
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Qy   1249 IGLGAFSSCYQAQDVGTGTLMAVKQVTYVRNTSSEQEEVVEALREIRMMSHLNHPNIIR 1308
           :|:|| || : ::|:|:           :|:|||      ||  ||   ||:::
Db    686 LGKGTYGIVYAGRDLSNQVRIAIKEI-----PERDSRYSQPLHEEIALHKHLKHKNIVQ 739

Qy   1309 MLGATCEKSNYNLFIEWMAGGSVAHLL-SKYGAFK--ESVVINYTEQLLRGLSYLHENQI 1365
           ||: +  : |::| : |||:: || ||: |   : |||:::| ||:|||:::|||
Db    740 YLGSFSENGFIKIFMEQVPGGSLSALLRSKWGPLKDNEQTIGFYTKQILEGLKYLHDNQI 799

Qy   1366 IHRDVKGANLLIDSTGQRLRIADFGAAARLASKGTGAGEFQGQLLGTIAFMAPEVL---- 1421
           :|||:|| |:||::   |:|:||| : |||        ||  ||:::
Db    800 VHRDIKGDNVLINTYSGVLKISDFGTSKRLA---GINPCTETFTGTLQYMAPEIIDKGP 855

Qy   1422 RGQQYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPGL 1481
           ||  ||:  : ||:: |:||:|| |||||    |  :||:   ::  :|
Db    856 RG--YGKAADIWSLGCTIIEMATGKPPF--YELGEPQAAMFKVGMFKVHPEIPESMSAEA 911

Qy   1482 RDVALRCLELQPQDRPPSRELL 1503
           :  |:|--|-|--|:|:||
Db    912 KAFILKCFEPDPDKRACANDLL 933
```

Search completed: December 20, 2002, 16:21:22
Job time : 34 secs